

searched: 283366 seqs, 96191526 residues

minimum DB seq length: 0
maximum DB seq length: 00000000

post-processing: Minimum Match 0% Maximum Match 100%

```
    2:  pir2;*
    3:  pir3;*
    4:  pir4;*
```

No. 18 is the number or results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query			DB	ID	Description		
		Match	Length	DB			%	2	-
1	1949	100.0	391	2	B70608		probable	PPE	probate
2	1656.5	85.0	396	2	H70741		probable	PPE	probate
3	1583.8	81.2	393	2	C70548		probable	PPE	probate
4	779.5	40.0	393	2	G70929		probable	PPE	probate
5	751.7	38.5	409	2	A70932		probable	PPE	probate
6	737.5	37.8	403	2	H70931		probable	PPE	probate
7	736.7	37.8	423	2	B70931		probable	PPE	probate
8	731.7	37.5	421	2	H87056		PPE-family	protein	
9	705.7	36.2	408	2	G70925		probable	PPE	probate
10	702.7	36.0	391	2	B70625		probable	PPE	probate
11	702.7	36.0	413	2	F70701		probable	PPE	probate
12	688.5	35.3	463	2	C70931		probable	PPE	probate
13	682.5	35.0	468	2	B70932		probable	PPE	probate
14	675.7	34.6	380	2	A70646		probable	PPE	probate
15	668.5	34.3	394	2	G70881		probable	PPE	probate
16	667.5	34.2	385	2	H70503		probable	PPE	probate
17	635.5	32.6	350	2	H70929		probable	PP3	probate
18	633.5	32.5	365	2	E70929		probable	PPE	probate
19	615.5	31.6	402	2	A70882		probable	PPE	probate
20	603.5	30.9	423	2	C70582		probable	PPE	probate
21	597.5	30.7	391	2	D70922		probable	PPE	probate
22	589.7	30.7	406	2	E70675		probable	PPE	probate
23	588.7	30.2	394	2	A70504		probable	PP3	probate
24	575.5	29.5	391	2	A70663		probable	PPE	probate
25	495.5	25.4	3300	2	D70575		probable	PPE	probate
26	473.5	24.3	180	2	G70834		probable	PPE	probate
27	452.5	23.2	3716	2	E70969		probable	PPE	probate
28	448.5	23.0	580	2	G70707		probable	PPE	probate
29	444.5	22.8	3446	2	H70874		probable	PPE	probate

ALIGNMENT S

RESULT 1

B70608 probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
C;Species: *Mycobacterium tuberculosis*
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_Change 22-Oct-1999
C;Accession: B70608
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Hahn, N.; Hedges, R.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentle, S.; Gentles, S.; Hamlin, N.; Hickey, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Whitehead, S.; Barrell, B.G.; Rajandream, M.A.; Barrell, B.G.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence
A;Reference number: A70500; PMID: 98295987; PMID: 96344330

A;Accession: B7006
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-391 <COL>
A;Cross-references: GB:293777; GB:AL123456; NID:93261726; PIDN:CA07839.1; PMID:15300000

C:/GeneID:1CS						
	A/Gene:	PPE	Query	Match	Score	Length
Best	Match	100.0%	Qy	100.0%	Score 1949;	391;
Local	Similarity	100.0%	D b	Pred. No. 3.5s-10s;	DB 2;	
Matches	391;	Conservative 0;	Qy	Mismatches 0;	Indels 0;	Gaps 0
1	MVDGFLPPEINSARMYAGPOSASLVAAMNWDSVASDLPSAASFQSIVWGLTVGSWIG	60				
1	MVDGFLPPEINSARMYAGGSASLVAAMQMDSVASDLPSAASFQSIVWGLTVGSWIG	60				
61	SSAGLMVAAASPVAVAMSVTAGQAEELTAQVRVAAAYETAGLTVPPIVIAERELMI	121				
61	SSAGLMVAAAPVAVAMSVTAGQALITAQVRVAAAYETAGLTVPPIVIAERELMI	121				
121	LIAATNLJGONTPAIAVNEAEYGMWAQDAAMFGYAAATATAATLTPBEEAPEMTSAGG	180				
121	LIAATNLJGONTPAIAVNEAEYGMWAQDAAMFGYAAATATAATLTPBEEAPEMTSAGG	180				
181	LIEQAAAVEEASTDAAANOLNNNQOALQOLAQPQTGTTPSSKGLWLKIVSPRSPISN	241				
181	LIEQAAAVEEASTDAAANOLNNNQOALQOLAQPQTGTTPSSKGLWLKIVSPRSPISN	241				
241	MVSMAANTHMSMTNSGYSMTNTLSNLKGFPAAAQQAVQTAQNGYRAMSSLGGSSLGSSG	300				
241	MVSMAANTHMSMTNSGYSMTNTLSNLKGFPAAAQQAVQTAQNGYRAMSSLGGSSLGSSG	300				
301	LGGGVANLGEAAVGSLSYQPAWAANQAVTPPARALPLTSLSAEEGPQMLGLGPV	366				
301	LGGGVANLGEAAVGSLSYQPAWAANQAVTPPARALPLTSLSAEEGPQMLGLGPV	366				
361	QMGAAAGGGGIVRUPPREYMPHS PAAG	391				

Dib 361 GQMARGAGGGLSGYLRRPPRYMPHSFAAG 391

RESULT 2

probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: H70741

R.; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; PMID:9634230

A;Accession: H70741

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-396 <COL>

A;Cross-references: GB:Z75555; GB:AL123456; PIDN:CAA99966.1; PID:e250360;

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: PPE

Query Match 81.2%; Score 1583; DB 2; Length 393;

Best Local Similarity 81.5%; Pred. No. 1.5e-86;

Matches 322; Conservative 20; Mismatches 47; Indels 6; Gaps 3;

Qy 1 MVDFGALPPEINSARMYAGPGSASLVAQQMWDVSASDLSASAFAQSUVWGLTVGSWIG 60

Db 1 MVDFGALPPEINSARMYAGPGSASLVAQQMWDVSASDLSASAFAQSUVWGLTVGSWIG 60

Qy 61 SSAGLMVAAASPYAWMSVTAGQAEELTAQVRVAAAAYETAYGLTVPPVIAENRAELMI 120

Db 61 SSAGLMVAAASPYAWMSVTAGQAEELTAQVRVAAAAYETAYGLTVPPVIAENRAELMI 120

Qy 121 LIATNLGQNTPAIVNEAEGYAAATAATATLIPFEEAPEMTSAGG 180

Db 121 LIATNLGQNTPAIVNEAEGYAAATAATLIPFEEAPEMTSAGG 180

Qy 121 LIATNLGQNTPAIVNEAEGYAAATAATATLIPFEEAPEMTSAGG 180

Db 121 LIATNLGQNTPAIVNEAEGYAAATAATLIPFEEAPEMTSAGG 180

Qy 181 LLEQAAVEEASDTAAANOLMNNVPQALQLAQOPTGTTPSSKLGGMKTVSPHRSPISN 240

Db 181 LLEQAAVEEASDTAAANOLMNNVPQALQLAQOPTGTTPSSKLGGMKTVSPHRSPISN 240

Qy 241 MVSMANNHNSMTNSGVSTMNTLSSMLKGPSAPAAQAVOTAONGVRAMSS---LGSSL 296

Db 241 VSSIANNHNSMMGTCGVSTMNTLSSMLKGSLAP-AAAQAVETAAENGWMASSLGSQLGSSL 299

Qy 297 GSSGLGGGVAANLGRAASYGSLSVQPAWAANQAVTTPARALPLTSLTSAAERGPQOMLG 356

Db 300 GSSGLGGGVAANLGRAASYGSLSVQPAWAANQAVTTPARALPLTSLTSAAQTAQPHMLG 359

Qy 357 GLPVGQMGARAGGGLSCVLRPPYPMHPHSPAG 391

Db 360 GPLGH-SVAGSGINNALRPARAYAIPRTPAG 393

RESULT 4

G70929 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Accession: G70929

R.; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; PMID:9634230

A;Accession: G70929

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-393 <COL>

A;Cross-references: GB:AL022021; GB:AU123456; PIDN:G3250699; PID:CPA17711.1; PID:e125460(

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: PPE

Query Match 40.0%; Score 779.5; DB 2; Length 393;

Best Local Similarity 43.7%; Pred. No. 4.3e-39;

Matches 179; Conservative 65; Mismatches 129; Indels 37; Gaps 10;

Qy 2 VDFGALPPEINSARMYAGPGSASLYAAQMWDVSASDLSASAFAQSUVWGLTVGSWIG 61

Db 1 VDFGALPPEINSARMYAGPGSASLYAAQMWDVSASDLSASAFAQSUVWGLTVGSWIG 60

Qy 62 SAGLMVAAASPYAWMSVTAGQAEELTAQVRVAAAAYETAYGLTVPPVIAENRAELMI 121

Db 62 SAGLMVAAASPYAWMSVTAGQAEELTAQVRVAAAAYETAYGLTVPPVIAENRAELMI 120

Qy 61 ASAAAEEAAYPYAWMSAAAQAOAAQTQARAAAEEAFAATVPPVIAANRASIMQL 120

RESULT 3

C70568 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Accession: C70568

R.; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; PMID:9634230

A;Accession: C70568

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

Qy	122 IATNLGONTPATAVNEAFYGEYAATAAAMFGEYAATAATATLIPFEAEPEMTSAGGL 181	Db	353 AAEAPGALFGEMALSSLAGRALAGTAVRSGAGAAARV 388
Db	121 ISTNVEFGQTSAAAAAYGEYAQDAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAQ 179		
Qy	182 LEQAAAVEPASDTAA--NOLMANNVPOQLQQLAQOPTCTPSSKLGLINK----- 229		
Db	180 GTQIAAVATAAGTAQSTLTEMITGLPNALQSNTSPQIQS-NGPLSMNWWLFGTPNPFPT 238		
Qy	230 -----TVSPHSPRSPIVNVSMAANHMSMTNSGYSMTNLSMLKGPAFAAAQAQVOTA 282		
Db	239 SISALTDQSLQPSFFYNTTEGLPYFSIGMNNFIOSAKTL-GHIGSAPAPA----AA 292		
Qy	283 QNGTRAMSLQSSLGSSGGVAANLGRASAISVSYLSPQAWAA-ANCAVTPAARALPQT 341		
Db	293 GDAKGLPLGGMIG---GGPVAAGLGNASVGKLYSPVWNSGPLGSVTFGAAPLFVS 348		
Qy	342 SLTSAEERGPQMLGGLPVQMGARAGGCLSGYLRVPPRYMPHSAAAG 391		
Db	349 TVSAAPEAAPGSLLGLP----AGAGGAGP-RYGFPTWMARPFAG 393		
	RESULT 5		
A70932	probable PPE protein - Mycobacterium tuberculosis (strain H37RV)		
C;Species: Mycobacterium tuberculosis			
C;Accession: A70932			
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome			
A;Reference number: A70500; PMID: 98295987; PMID: 9634230			
A;Accession: A70931			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-403 <COL>			
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17728.1; PID:e125461			
C;Genetics:			
A;Gene: PPE			
	RESULT 6		
H70931	probable PPE protein - Mycobacterium tuberculosis (strain H37RV)		
C;Species: Mycobacterium tuberculosis			
C;Accession: H70931			
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome			
A;Reference number: A70500; PMID: 98295987; PMID: 9634230			
A;Accession: A70932			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-409 <COL>			
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17729.1; PID:e125461			
C;Genetics:			
A;Gene: PPE			
	RESULT 7		
B70931	probable PPE protein - Mycobacterium tuberculosis (strain H37RV)		
C;Species: Mycobacterium tuberculosis			
C;Accession: B70931			
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome			
A;Reference number: A70500; PMID: 98295987; PMID: 9634230			
A;Accession: A70931			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-409 <COL>			
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17729.1; PID:e125461			
C;Genetics:			
A;Gene: PPE			
	Query Match 38.5%; Score 751; DB 2; Length 409;		
Best Local Similarity 44.7%; Pred. No. 2.0e-37;			
Matches 177; Conservative 53; Mismatches 13; Indels 28; Gaps 10;			
Qy	2 VDFGALPPEINSARMYAGGGSASLIVAAQNWDSVASDLFSAASAFQSIVWGTIVGSWIGS 61	Db	223 RLGGMKTKVSPHERSPI SNMVSMAHMMSMTNSGYSM-TNTLS---SMLKFAPAAAQAV 278
Db	1 MDFGALPPEINSCRMAYAGGGSQPLAAAAWDAALAAEYSAASYGSTIEGLTVAPMGP 60	Qy	182 LEQAAVEEEASDTAA----NQMVNVQALQOQLPQQT-----TPSS 222
Qy	62 SAGIMVAAASPYAAMWSTAGQAAELTAACVRVAAAAYETAYGLTVPPPVIAANRAELMIL 121	Db	184 AAQSAJIAHTGASAGAQQTTSLSQIAAIISVLQGSSSSTAATAGPSGLLGLIVGSGSS 243
Db	61 SSITMAAAAPYYAWISTAGQAEQAAQKIAQVYETAAFAATVPPVIEANRALLMSL 120	Qy	223 RLGGMKTKVSPHERSPI SNMVSMAHMMSMTNSGYSM-TNTLS---SMLKFAPAAAQAV 278
Qy	122 IATNLGONTPATAVNEAFYGEYAATAAAMFGEYAATAATATLIPFEAEPEMTSAGGL 181	Db	244 WLDKLMLDDN-----SNPNTIAASSGLLPSPNTIAFPFLGLGGVAAADAGDV 293
Db	121 VATNFGONTPATAAATEAYWAQDAAMYGSSATA-SQLAPESEPPQTNNSAT 179	Qy	279 QTAAGONGVRAMSSLGSSSL----GSSGLGGCVAANI GRAASVGSLSVFOQAWAAAANOAVTP 333
Qy	182 LEQAAAVEPASDTAA----NQLMNNVPOQLQQLAQOPTQGTTPSKSKLGLWKTYSPH 234	Db	294 LGEATG----GLGEATG----GLGEATVAPLGSQGLGGLGTVAAAGLGNAAATVGTVLSVFPWTAAAPLASP 348.
Db	180 AACQSAVVAAGAAASSDITAOIQLSQLISLSPSTIQLSA-TPATATSAASAG-WDTV-- 232	Qy	334 AARAL--PLTSLTSAERAEGPQGMUGGLPVQGMGARAGGGISLGVLRVPP---RPYVMFH 386
Qy	235 RSPSNMVSMAHMMSMTNSGVS----MTNTLSSMLKGFPAAAQAVQTAQNGYRAM 289	Db	349 LGSALGGTPTWAPPAPPVAAG---MEGMPFTGMGQGFG----RAVPOYGFRENVAR 398
Db	233 LOSITLILNLGPYSTIICLGLAQNAPQEVAAAGKLAAGALSP 292	Qy	387 SPAAG 391
Qy	290 SSL-GSSLSS-SGJGGYVAANLGRASAISVSYLSPQAWAAQVTPAARALPULTSLSA- 346	Db	399 PPAG 403
Db	293 APLRGGYGIDPLGGGATGGIARAYIVGSLSPQGHAAAPMVRAYASVLPGTGAAPAL 352		
Qy	347 AERSPGQMLGGLPVQGMGARAGGGL---SGYLRV 377		

A;Author:	Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title:	Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number:	A70500; MUID:9825987; PMID:9634230
A;Status:	Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type:	DNA
A;Residues:	1-423 <COL>
A;Cross-references:	GB:AL022021; GB:Ali123456; NID:93250699; PIDN:CAA17722.1; PMID:e125461
A;Experimental source:	strain H37RV
C;Genetics:	
A;Gene:	PPE
Query Match	37.9%; Score 716; DB 2; Length 423;
Best Local Similarity	41.8%; Pred. No. 1.8e-36;
Matches	182; Conservative 50; Mismatches 123; Indels 80; Gaps 12;
Db	1 MDFGALPPEINSARMYAGPSASLVAARQMNDSVASDILFSAASAFQSVVWGLTVGSWIG 60 1 MDFGALPPEINSARMYAGPSASLVAARQMNDSVASDILFSAASAFQSVVWGLTVGSWIG 59
Qy	2 VDFGALPPEINSARMYAGPSASLVAARQMNDSVASDILFSAASAFQSVVWGLTVGSWIGS 61
Db	1 MDFGALPPEINSARMYAGPSASLVAARQMNDSVASDILFSAASAFQSVVWGLTVGSWIGS 59
Qy	62 SAGLMVAAASPYAWMSVTAGAELTAQVRVAAAAYETAYGLTVPPVIAENRAELMI 121
Db	60 SSTMASASAPYAWMSVTAGAELTAQVRVAAAAYETAYGLTVPPVIAENRAELMI 119
Qy	122 IATNLGONTPAIAVNEAEYGENWAQDAAMFGYAAATAATATLIPFEAPEMTSAGGL 181
Db	120 IATNLGONTPAIAVNEAEYGENWAQDAAMFGYAAATAATATLIPFEAPEMTSAGGL 180
Qy	121 LIATNLGONTPAIAVNEAEYGENWAQDAAMFGYAAATAATATLIPFEAPEMTSAGG 180
Db	120 LIMSNIFGQNSTAIAKEAYTENWMIQDRAAMTSYQASVLEAVGATKFTAPPLGVNEVG 179
Qy	181 L-----LLEQAAVEEASDTAAQMLNN-----VPQALQQ---LAQP 214
Db	180 LAQEVEEVVEEVVEEVVEAEQASQAAALDQAVNEGMETAVPVQDVQVNVDATP 239
Qy	215 TQGTPSPSKGG--IWKTVSPHRSPISNVMSMNTLSNLKGPPA 272
Db	240 QTAVDSSAAPQLWGGAQHLSPINDTLSMNNHAGMANAGSLVNGMGSAMKSLAP- 298
Qy	273 AAAAQVQTAQONGVRAMMSLGSIGSGGAAVNLGRAASVGSLSVPOAWAAANGAVT 332
Db	299 TTTRAAESAFAMGSAVQSTGRLLGSSGGHVTQQLRRAASIGSLRPQTWTMASQPT 358
Qy	333 PAARALPLTSLTAAERGCQML-GGLIVPGQM---GARAGGGISGVLRVPPREYVMHSP 388
Db	359 AATRALSPARAVATESASEPLGGGLMAPMVPGGGGTGGVNTALLQPRAFVMPNP 418
Qy	389 AAG 391
Db	419 AAG 421
RESULT 9	
G70925	Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species:	Mycobacterium tuberculosis
C;Accession:	G70925
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	
Nature 393, 537-544, 1998	
A;Authors:	Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title:	Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number:	A70500; MUID:9825987; PMID:9634230
A;Accession:	G70925
A;Status:	Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type:	DNA
A;Residues:	1-408 <COL>
A;Cross-references:	GB:Z74024; GB:AL123456; NID:93250700; PIDN:CAA98377.1; PMID:e1301025;
C;Genetics:	
A;Gene:	PPE
RESULT 8	
H87056	PPE-family protein [imported] - Mycobacterium leprae
C;Species:	Mycobacterium leprae
C;Accession:	H87056
R;Cole, S.T.; Eiglemeir, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hegg, R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Hamlin, N.; Holroyd, S.; Seeger, K.; Simmonds, M.; Skelton, J.; Squares, R.; Squire, M.A.; Reference number: A86909; MUID:21128732; PMID:11234002	
Nature 409, 1007-1011, 2001	
A;Authors:	Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squire, M.A.; Reference number: A86909; MUID:21128732; PMID:11234002
A;Title:	Massive gene decay in the leprosy bacillus
A;Accession:	H87056
A;Status:	Preliminary
A;Molecule type:	DNA
A;Residues:	1-421 <STO>
A;Cross-references:	GB:AL450380; NID:913093150; PIDN:CAC31563.1; GSPDB:GN00147
C;Genetics:	
A;Gene:	ML1182
Query Match	37.5%; Score 731; DB 2; Length 421;
Best Local Similarity	41.1%; Pred. No. 3.5e-36;
Matches	174; Conservative 55; Mismatches 160;
Db	122 IATNLGONTPAIAVNEAEYGENWAQDAAMFGYAAATAATATLIPFEAPEMTSAGGL 181 121 VATNFFGQNTPAIAVNEAEYGENWAQDAAMFGYAAATAATATLIPFEAPEMTSAGGL 179
Qy	182 LEQAAA-----VEASDTAAQMLNN-----VP-QGTTPSKLU---

RESULT 11
 Db 180 AGQQAAATVSSTVPEPLATAAVPQLCOLSTSLLPWSALQWIAENILGLTPDNRMTIV 239
 Qy 225 -----GGLWKTVPSPRSPEMNVMANNNSMNTGSVSMNTLSSMKGFAPAAA 275
 Db 240 RILLGTSYFDEGL-----LQEASLQQNLPGTGAG--DGSVSLDWSWPFTIA 287
 Qy 276 QAVCTAAQNGVRAMSSL-GSSLGS-----SGUGGVAANLGRAASVGSLS 319
 Db 288 -----GPRAPSVAQGGAVQYWTQMYWALDRSTIGSVSAAAGKGSAGSLS 338
 Qy 320 VPOQAWAAAOVATPAARALP---LTSLTSAEERGPOMLGLPVONGARAGGGLSGVLR 376
 Db 339 VPPDMAARRWANDAARWLPDDVTALRGTAENA---LJRGFPMASAGQSTGGF--VHK 393
 Qy 377 VPPRPPYMDPHSPAG 391
 Db 394 YGFRLAVMDPFPAG 408

RESULT 12
 Db B70625
 Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Accession: B70625
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; PMID:38295387; PMID:9634230
 A;Accession: P70560
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Cross-references: GB:Z85436; GB:AL123456; NID:93261770; PIDN: CAB08826.1; PID:e316565; E;
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: PPE

Query Match 36.0%; Score 702; DB 2; Length 413;
 Best Local Similarity 39.1%; Pred. No. 1..e-34;
 Matches 168; Conservative 6; Mismatches 145; Indels 56; Gaps 7;

Qy 1 MVDFGLALPPETNSARMYAGPGSASLIVAAQMQWDVSADLSFSAAGAFQSYYWGLTIVGSWIG 60
 Db 1 MLDFDALOLPPETNSALMYAGPGSMPMLAAWEALAELOQTASTYDALITGLADGPWQG 60
 Qy 61 SSAGLIVAAASPYAAMMSVTAGQALTTAQVRAAAAYETAYGLTVPPPYIAENRAELMI 120
 Db 61 SSAASVAAATPQVWLRSQAOAQGSAVAAASAAFFATVPPPEIAANRAELMA 120
 Qy 121 LLATNLGONTPAIVNEAEGWMAQDAAMFGTAATAATALLPFEAPEPTISAGG 180
 Db 121 LLATNLGONTAAIAATEQYAEMTAQDAAMNYGYAGASAATQSPNPAAQTINPAG 179
 Qy 181 LLEQAAVEEEASDAAQANOLMANNYQOALQOQAOPQGTTPSKLLGWLTKVSPHRSPISN 240
 Db 180 LASQASVGQAVSGANAQNLTDFKL-----FGLSGIFPNEPWLTDLGK 226
 Qy 241 MVSMANHMSMTNSGYSMTLSSMLKGFPAPA---AAQAVCT-----
 Db 227 ALGLTGHWTSDGSGLIVGGVLGDVQGVTGSABLDASYAMDTEFKWVSPARLMVTFKD 286
 Qy 281 -----AQNQVBRMSSLOSSGLGGVAAANIGRASVGSLSUPQA 323
 Db 287 YFGLAHDLPKWASEGKAAGEAAKALPAAPVPSAGL-SGVAGAVGQQAASVGKPKAV 345
 Qy 324 WAAANGAVTPAARALPLTSLTSAAERGPOMIGGLPVONGARAGGGLSGVL--RVPFRD 381
 Db 346 WTATTFAASAVLALSGNLGAAAAEGSTHAFGMPFL-MGSGGGRAPFINFAAPRYGKPF 403
 Qy 382 YVMPHPAAAG 391
 Db 404 TVIAQPFPAGG 413

RESULT 12
 C70931
 Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Accession: C70931
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

RESULT 13
 Qy 237 P--ISNNVSMANNMS-MTNSGYSMTLSSMLKGFPAPAALQAVTAQVRAANSSLG 293
 Db 240 TPPVANILINSVNTAAVYNAALPTAFLANALNSGAPVAFLEGATEAEG--AASAAA 296
 Qy 294 SSLGSSGCGGVAANLGRAASVGSLSVFOQAWAANQATTAAPATTAGTATELEGSSWTVAEEA-GP 353
 Db 297 AGLADSVTPEAGLGSVLRPFRYMP 385
 Qy 354 MLGGLPVGCGMGRAGGGLGSVLRPFRYMP 385
 Db 356 VTRGMP-GMASAKGTGAWAGPRYGFESTVMP 386.

A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-463 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17723.1; PID:e125461
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: PPE

Query Match 35.3%; Score 688.5; DB 2; Length 463;
Best Local Similarity 42.8%; Pred. No. 1.3e-33;
Matches 174; Conservative 48; Mismatches 136; Indels 49; Gaps 11;

Qy 62 SAGLMVAASPYAWMSVTAGQELTAQVRVAAAYETAYGLTVPPVIAENRAELMIL 121
Db :
Db 61 SSAGMAAAAPAAPYTWMSGTSAAQAKAADARAAVAVAYTAFAAVVUPPOIAANRSQJSL 120

Qy 122 IATNLGONTPALAVNEAYGENWAQDAAMFGYAAATAATATATLPLPEEAPMTSAGGL 181
Db :
Db 121 VATNIFGQNTAAATEAEEYGENWAQDYNAMFGYASSDATA-SRLTPTAPPOTNPGSL 179

Qy 182 LEQAAYVEERAS-----DTAAANQMNVPDALQOLAQOPLQTTPSKLGGGL- 227
Db :
Db 180 AGQAAATGQATALLASGTINAVTAAQFQFDPDIPFLQGIA-TIYSTQYQLM6QOLI 237

RESULT 14

Qy 228 -----WIKTVSPHRSPISTMVSMANNHMSMTNSGVSMNTLSSMLKGFPAPAAAQ 276
Db :
Db 238 NAIFGPTGATTYQNVFVTANVTKPSTVANDANSAPNLMTEFKVF----WQPPPAPE 291

Qy 277 AVQTAQAGVYTRANSSLGSILG----SSCLGGVAAANTGRAAFYGSLSVPQWAAANQAV 331
Db :
Db 292 IPK-----SSLGAGIQLRSLGSLAHAASAGUQANLYGDLISVPPSWASATPAV 341

Qy 332 TPAARALPLTSLTSA-AERGPQWMLGGLPQMGNGARAGGGL 371
Db :
Db 342 RLVANTLPATSLAAPATQIPANLQOMALGSM--TGGAL 379

C;Species: Mycobacterium tuberculosis
C;Accession: A70646
R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome;
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70646
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <COL>
A;Cross-references: GB:Z838867; GB:AL123456; NID:93261695; PIDN:CAA062278.1; PID:e291015; I
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: PPE

Query Match 34.6%; Score 675; DB 2; Length 380;
Best Local Similarity 43.1%; Pred. No. 6.2e-33;
Matches 172; Conservative 56; Mismatches 143; Indels 28; Gaps 12;

Qy 2 VDFGALPBEINSARMYAGPGSASLIVAAQMWDVSASLAAAFOSTVWGLTVGSNIGS 61
Db :
Db 1 MDFALPPEINSARMYAGPGSASLAAEATTAAYGSLISGLAHLNFGP 60

Qy 62 SAGLMVAASPYAWMSVTAGQELTAQVRVAAAYETAYGLTVPPVIAENRAELMIL 121
Db :
Db 61 AAESMAVTAAPYGMLYTAEKTOQTAICARAALAFEOAYANTLPPVVAANRIQLAL 120

Qy 122 IATNLGONTPALAVNEAYGENWAQDAAMFGYAAATAATATLPLPEEAPMTSAGGL 181
Db :
Db 121 VATNIFGQNTAAATEAEEYGENWAQDYNAMFGYASSDATA-SRLTPTAPPOTNPGSL 179

Qy 182 LEQAAYVEERAS-----DTAAANQMNVPDALQOLAQOPLQTTPSKLGGGL- 228
Db :
Db 180 TAQRRAVSSQATDPLSL-LIETVQQLQALTIPEFIPDETFELDAIFGYATVGTCVDE 237

RESULT 15

Qy 239 SNMVSM--ANHMNTNSGVSMNTLSSMLKGFPAPAAAQAVTAQNGVRAMNSLGSGL 296
Db :
Db 238 SFVAGTIGAESNLGVGDENPAEVTPCDGFIGELVSA---TSPGGVVA-SGAG-- 289

Qy 2 VDFGALPBEINSARMYAGPGSASLIVAAQMWDVSASLAAAFOSTVWGLTVGSNIGS 61
Db :
Db 1 MDFGLQPPETSGEMYLGGAGPMIAAAVAVDGLAAELOMASVASEWSLGP 60

Db 299 GAASVGNNTLASVGRANSIGLSPVPPSWAAPSTRPVSAASPAGLTLIPLGTDVAEHGMPG- 348
 Qy 354 MLGGIPVGOMGARAGAGGGLGSVGL-RVPFRPYVMHSPAG 391
 Db 349 -VPGPV-----AAGRASGVLFYGVRLTMHHPAG 380

RESULT 15

G70881 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C;Accession: G70881
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentle, S.; Hamlin, N.; Holroyd, S.
 Randal, M.A.; Rogers, J.; Rutten, S.; Seeger, K.; Stelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Soares, P.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; PMID:98255987; PMID:9634230
 A;Accession: G70881
 A;status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-394 <COL>
 A;Cross-references: GB:AL008967; GB:AU123456; MID:93261491; PID:CAA15564.1; PID:e117389
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: PPE

Query Match	34.3%	Score	668.5	DB	2	Length	394	;
Best Local Similarity	40.8%	Pred.	No. 1	1.6-32	;			
Matches	161;	Mismatches	156;	Indels	17;	Gaps	7;	
Matches	161;	Conservative	61;					

Qy 2 VDFGALPPIINSARMYAGGGSASILVAAQMMDSVAVASAFQSYVWGLTVGSWIGS 61
 Db 1 MDPGALPPIINSRYAGGAAPIMAAGTQNLAVELSTTASSVESVIMQTTTEQWLGP 60

Qy 62 SAGIMVAAMSPYAWMSUTAGQELTAQVRVAAAYETAYGLTVPPPVIAENRAELMIL 121
 Db 61 ASMVMVVAAPYLAWLYTAESAAHAAQAMAAAFAFANTVPEAVANRALLAAL 120

Qy 122 IATNLLGQNTPAIAVNEAFTGEWAQDAAMFGYAAATAATATLIFEEABMTSAAGL 181
 Db 121 VATNVLGQNTPAIMATEAHYGEWAQDALAMGYAASS-AAGRINLPLITPSQTANMAGL 179

Qy 182 LEQAAVEREASDAAANO---LMNNVYQALQQLAQTPGTIPSSKLGKJNKTVPSP--H 234
 Db 180 AGQAIAVSIAAAASTVQQIGLSLISNEDNAVNGFASPLITSADAAGIGI-QDIEBLG 239

Qy 235 RSPISNNMSMANHMSMTNSGSMNTLSMLKGFAAAAAQAVQTAQNGY--RAMS 291
 Db 240 ITFYQNAINGAVN---TIAFWFMATIPAVFLGHAFALNPATVAAADAVPAAAAG 295

Qy 292 LGSSLGSSGLG-GVAAAGLGRASVGSLSVPQWAAAQNQAVTFAAARLPLTLSAERG 350
 Db 296 LAHTVTPVGVGASLTASIGEASSVGGLSVPAWSSTAAPMTSGTTALEGSSWAVPPEAG 355

Qy 351 PGQMUGGLPVQGMARAGGGLGSVLRVPPRPYWP 365
 Db 356 PVAAAMPGM-AGISGAAKGNAYAGPRYGFKPITMP 369

Search completed: August 25, 2004, 03:13:46
 Job time : 41 secs

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GenCore - protein search, using sw model			
Copyright (c) 1993 - 2004 Compugen Ltd.			
on:			August 25, 2004, 03:05:03 ; Search time 118 Seconds (without alignments)
in on:			1045.488 Million cell updates/sec
title:			US-09-724-685-107
perfect score:			1949
sequence:			I MVDGFALPPEINSARMYAGP.....SGVLRVPPRYPVMPPSPAAG 391
oring table:			BLOSUM62
Gapop			10.0 , Gapext 0.5
arched:			1017041 seqs, 315518202 residues
total number of hits satisfying chosen parameters:			1017041
minimum DB seq length:			0
maximum DB seq length:			2000000000
first-processing:			Minimum Match 0% Maximum Match 100%
Listing first 45 summaries			r
atabase :			SPREMBL_25: 1: sp_archea;* 2: sp_bacteria;* 3: sp_fungi;* 4: sp_human;* 5: sp_invertebrate;* 6: sp_mammal;* 7: sp_mnd;* 8: sp_organelle;* 9: sp_phage;* 10: sp_plant;* 11: sp Rodent;* 12: sp_virus;* 13: sp_vertebrate;* 14: sp_unclassified;* 15: sp_rvirus;* 16: sp_bacteriopl;* 17: sp_archeap;*
score:			SPREMBL_25: 1: 1949 100.0 391 16 0052988 2 1920.5 98.5 390 16 Q7U0E9 3 1779.5 91.3 396 16 Q7U0T1 4 1648 84.6 393 16 Q8VIZ3 5 1583 81.2 393 16 006341 6 1583 81.2 393 16 Q7TWFS 7 779.5 40.0 411 16 053939 8 779.5 40.0 411 16 Q9QK11 9 754 37.8 410 16 053957 10 751 38.5 409 16 Q7T2H7 11 749 38.4 409 16 Q7T2H7 12 740.5 38.0 399 16 Q7T2H8 13 737.5 37.8 403 16 053956 14 736 37.8 423 16 053950 15 736 37.8 423 16 P71869 16 731 37.4 421 16 Q7T2I4 17 702 36.0 391 16 P96362 18 702 36.0 391 16 Q7U0T5 19 683.5 35.0 413 16 006386 20 682.5 35.1 694 16 Q8VJW0 21 682.5 35.0 688 16 053958 22 675 34.6 380 16 P95190 23 675 34.6 380 16 Q7TX66 24 670.5 34.4 385 16 Q7T2R7 25 669.5 34.4 394 16 Q7TXX5 26 668.5 34.3 462 16 Q33310 27 667.5 34.2 385 16 Q3204 28 666.5 34.2 385 16 Q8VJZ0 29 641 32.9 364 16 Q7T2J5 30 637 32.7 350 16 Q7T2J2 31 635 32.6 363 16 Q53940 32 633.5 32.5 365 16 Q86373 33 629.5 32.3 405 16 Q8VJW5 34 626.5 32.1 381 16 Q7TX67 35 618.5 31.7 397 2 Q9AF0 36 615.5 31.6 382 16 Q7TXX3 37 615.5 31.6 402 16 Q33312 38 610 31.3 443 16 Q8VJK9 39 604 31.0 443 16 Q7U242 40 603 30.9 423 16 Q7U114 41 603 30.9 426 16 Q05907 42 597.5 30.7 391 16 Q05798 43 594.5 30.5 391 16 Q7TX76 44 589 30.2 406 16 P71869 45 589 30.2 406 16 Q7Tw99
ALIGNMENTS			
RESULT 1			
005298			PRELIMINARY;
ID 005298;			PRT; 391 AA.
AC			
DT 01-JUL-1997 (TREMBLrel. 04, Created)			
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Hypothetical protein (PPE family protein).			
DE RV196 OR MTIC364-08 OR MTIC34.			
GN Mycobacterium tuberculosis.			
OS			
RA Davies K., Devlin K., Jagels K., Krogh A., McLean J., Molle S., Murphy L.,			
RA Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekala F.,			
RA Gordon S.V., Eigeneimer K., Gas S., Connor T., Connor R.,			
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor N., Holroyd S.,			
RA Davies K., Davies R., Devin K., Skelton S., Squares S., Squares R.,			
RA Hornsby T., Osborne J., Qual M.A., Rajandream M.A., Rogers J.,			
RA Oliver S., Osborne J., Skelton S., Whiteheads S., Barrell B.G.;			
RA Sulston J.B., Taylor K., Whiteheads S., Barrell B.G.;			
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";			
RL Nature 393:537-544 (1998).;			
RN [1].			
RN SEQUENCE FROM N.A.			
RN STRAIN=CDC 1551 / Oshkosh;			
RN Peterkin J.F., Allard D., Eisen J.A., Carpenter L., White O.,			
RN Petersen J., DeBoer R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RN Kolonay J.F., Nelson W.C., Umayam L.A., Ermoljeva M.D., Salzberg S.L.,			
RN Bishai W.;			
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";			
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
SUMMARIES			
%			
SUIT No.			
Score			
Query			
Match			
Length			
DB ID			
Description			
005298 mycobacteri			
Q7U0E9 mycobacteri			
Q7U0T1 mycobacteri			
Q8VIZ3 mycobacteri			
Q06341 mycobacteri			
Q7TWFS mycobacteri			
Q7T2H7 mycobacteri			
Q7T2H8 mycobacteri			
Q53956 mycobacteri			
Q53950 mycobacteri			
Q7T2I4 mycobacteri			
Q9Z5K0 mycobacteri			

RESULT 6						
Db	Q7TWF5	PRELIMINARY;	PRT;	393 AA.		
Qy	Q7TWF5; DT 01-OCT-2003 (TREMBrel 25, Created)					
Db	DT 01-OCT-2003 (TREMBrel 25, Last sequence update)					
Qy	DT 01-OCT-2003 (TREMBrel 25, Last annotation update)					
Db	DE PE Family protein.					
Qy	GN PPE60 OR MB3305.					
Db	OS Mycobacterium bovis.					
Qy	OC Bacteria; Actinobacteria; Actinomycetida; Actinomycetales;					
Db	OC Corynebacteriales; Mycobacteriaceae; Mycobacterium.					
Qy	NCBI TaxID=1765;					
Db	RN [1]					
Qy	RP SEQUENCE FROM N.A.					
Db	STRAIN=Af2122/97;					
Qy	RX MEDLINE=22703107; PubMed=12788972;					
Db	RA Garnier T., Englemeier K., Camus J.-C., Medina N., Mansoor H.,					
Qy	RA Pryor M., Dutchoir S., Grondin S., Lacroix C., Monsenpe C., Simon S.,					
Db	RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,					
Qy	RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,					
Db	RT "The complete genome sequence of <i>Mycobacterium bovis</i> .";					
Qy	RA Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).					
Db	RL EMBL; BX248346; CAD95622.1; -.					
Qy	DR Complete Genome.					
Db	SQ SEQUENCE 393 AA; AF4C20C95DAE7DD4 CRC64;					
Qy	Query Match 81.2%; Score 1583; DB 16; Length 393;					
Db	Best Local Similarity 81.5%; Prod. No. 9.3e-82;					
Qy	Matches 322; Conservative 20; Mismatches 47; Indels 6; Gaps 3;					
Qy	1 MVDFGALPPBEINSARMYAGPSASLVAQMDVASDLFSASAFOSVVWGLTVGSWIG 60					
Db	1 MVDFGALPPBEINSARMYAGPSASLVAQMDVASDLFSASAFOSVVWGLTVGSWIG 60					
Qy	61 SSAGIMVAASPYFVAMSVTAGQELTAQVRAAAYETAYGLTVPPVIAENRAELMI 120					
Db	61 SSAGIMVAASPYFVAMSVTAGQELTAQVRAAAYETAYGLTVPPVIAENRAELMI 120					
Qy	121 LIATNLIGONTPATAVNEAEYGMWAQAAAMEGYAATAATATAATLPPPEAPENTSAGG 180					
Db	121 LTATNLIGONTPATAEANQDAYSQWDQAEMYGAATAATATAATLPPPEAPLTPNPGG 180					
Qy	181 LLQQAAVVEAISDTAAQOLMNNTVPOAQQLQOPTGTTPSSKLGILWKTVSPHSPISN 240					
Db	181 LLQQAAVVEAISDTAAQOLMNNTVPOAQQLQOPTGTTPSSKLGILWKTVSPHSPISN 240					
Qy	181 LLQQAAVVEAISDTAAQOLMNNTVPOAQQLQOPTGTTPSSKLGILWKTVSPHSPLSN 240					
Db	241 MVSMANNHMSMTNGVSMTNTLSSMLKGFAPIAAAQVTAQNGTYRAMSS---LGSSL 296					
Qy	241 VSSANNHMSMMGTGVSMNTNLHSMLGKLP AAAQVETARENGWAXSSLQGQSSL 299					
Db	297 GSSGGGGVAAVLGRAASVGSLSVPOAWAAANCAVTPAARALPLTSAAERGQCOMLG 356					
Qy	300 GSSGGGAGAAVLGRAASVGSLSVPOAWAAANCAVTPAARALPLTSAAERGQCOMLG 359					
Db	357 GLPVQMGARAGGGLSGYLVRPPRPPYMPHSPAAAG 391					
Qy	360 GLPLGH-SVNGASSINNALRVPARAYA1PRTPAG 393					
Db	DT 01-OCT-2003 (TREMBrel 25, Created)					

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin J., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skerrett S., Squares S., Sturt R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence," *Nature* 393:57-54 (1998).

[2] SEQUENCE FROM N.A.

RC STRAIN=CDCC 1551 / Oshkosh; Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwynn M., Haft D., Hickey E., Kolonay J.P., Nelson W.C., Umamaheshwar P., Salzberg S.L., Ermoljeva M., Utterback T., Weidman J., Khouri H., Mikula A., Bishai W.;

RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR AL022021; CAA17711.1; ALT_INIT.

DR AE007043; AAK46108.1;

DR PIR; G70929; G70929.

TIGR: MT1838; -;

DR Tuberculist; PV1789; -;

DR InterPro; IPR000030; Microbac_PBE.

DR PF00823; PBE; 1.

KW Complete proteome.

SEQUENCE 41 AA; 40557 MW; 03C90B5E05030B7DA CRC64;

Query Match 40.0%; Score 779.5; DB 16; Length 411;

Best Local Similarity 43.7%; Pred. No. 2.1e-36;

Matches 179; Conservative 65; Mismatches 129; Indels 37; Gaps 10;

SQ 2 VDGFALPPEINSARMYAGPGSASLVAANQQMDSVASDLFSSASAFAQSQVWGLTVGSWIGS 61

Db 19 MDGFALPPEINSARMYAGPGSASLVAANQQMDSVASDLFSSASAFAQSQVWGLTVGSWIGS 61

Qy 62 SAGIMVALAASPYIAWMSVTAQGQELTAAQVRVAAAAYETAYGTVPVVENRAEMIL 121

Db 79 ASAAMAEEAWPYAAWMSAQAQEQQATOARAQAAAEEAFAATVPPPLIAANRASIMOL 138

Qy 122 IATNLLGONTPATAVNEAEYGENWAQDAAMRGYAAATAATATATLIPFEAPEMTSAGGL 181

Db 139 1STNVEFGQTSAAAAEEYGENWAQDAAMAYAGSSASA-VTPFSTPPQIANPTAQ 197

Qy 182 LEQAAAEEASDTAA- -NOLMNINVPQALQQLAQOPTGTTPSKLGIWK-----

Db 198 GTQAAVAAVAAQTAQSTIEMITGLPNALQSTSPLQS-NGPLSLTWQLFGTNEPT 256

Qy 230 -----TWSPHSPISPINMVSANNMNSMTNSGVSMNTLISSMLKGFPAAAQAYQATA 282

Db 257 SISALLTDIOPYASFFXTYEGLPYFSIGNNNFIQSARTL-GLGSSAAPRA----AA 310

Qy 283 QNGYRAMSSLGSISGIGGYAANLGRASAISVGSLSVPAQWA-ANOQAVTPAARALPLT 341

Db 311 GDAAKGLPQLGGMIG---GGPYAAGLGNAAISVGKLSVPPWMSGPLPSVTPGAAPLVs 366

Qy 342 SLTSAAERGPQGMQLGGLPVGCMGARAGGGSLGVLPYRPMYHPSAAG 391

Db 367 TVSAAPEAAGPSLIGGLP---AGAGGAGAGP-RYGFPTVMARPPFG 411

RESULT 10

Q99Q11 PRELIMINARY; PRT; 409 AA.

AC Q99Q11; PRELIMINARY; PRT; 409 AA.

DB 01-JUN-2001 (TREMBLrel. 17, Created)

DB 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DB 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DR PPE-family protein.

DR RV1808 OR MTW049-30.

DR Mycobacterium tuberculosis.

OC Corynebacteriaceae; Actinomycetales; Mycobacterium.

OC Bacteria; Actinobacteria; Actinomycetales; Mycobacterium.

OC Corynebacteriaceae; Mycobacterium.

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=H337RV;

RX MEDLINE=98295987; PubMed=9634230;

RX Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Barnham D., Brown D., Chillingworth T., Connor R., Davies R., Devinlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Krogh A., McLean J., Moulie S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squires R.,

DR Rv1808 OR MTW049-30.

DR RV1808-1-like protein.

DR MYC1808 OR Q99Q11.

OS Mycobacterium microti.

OC Bacteria; Actinobacteria; Actinomycetales; Mycobacterium.

OC Corynebacteriaceae; Mycobacterium.

OC NCBI_TaxID=1806;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=myco 94-272, and OV254;

RA Sivason V., Heym B., Mazancourt P., Gaillard J.-L.L.;

RA "PPE_Rv1808 orthologue of Mycobacterium microti";

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF35180; AAC20893.1; -;

DR IntePro; IPR00030; Microbac_PBE.

DR Pfam; PF00823; PBE; 1.

DR SEQUENCE 410 AA; 40044 MW; 3B9DA3174655A5EA CRC64;

Query Match 38.7%; Score 754; DB 2;

Best Local Similarity 44.5%; Pred. No. 5.7e-35;

Matches 177; Conservative 51; Mismatches 140; Indels 30; Gaps 10;

Db 1 MVDFGALPPEINSARMYAGPGSASLVAANQMWDSVASDLSAASFQSYVWGLTVGSWIGS 60

Db 1 MLDFGALPPEINSGRMYAGPGSGPLAAAGDALAELYSAASAYSIGSIEGLTVAPWNG 60

Qy 61 SSAGIMVAASPSVWMSVTAGQELTAACVRAAAYTAYGTVPVPPVIAERAEIMI 120

Db 61 PSSTIVMAAAYPYAVWISVTAGQEAOQAGQAKLAGVTEATATVPPVTEANRALLNS 120

Qy 121 LIATNLLGONTPATAVNEAEYGENWAQDAAMFGYAAATAATATLIPFEAPEMTSAGG 180

Db 121 LVATNLLFGQNTPATATEHYAENWAQDAAMYGAQSSATA-SQLAPESEPPQTNPA 179

Qy 181 LLEQNAAVEEASDYYAA-----NQLMNVQDQLQALQOPTQCTTPSSKLGILWKTIVSP 233

Db 180 TAAQSAAVVAQAGAASSDITAQLSOLISLPLSTQSLA-TTATATASAG--WDTV - 233

Qy 234 HRSPISNVVANNMISMNSGV--SMNTLSSMLKGPAALAQAQVTAAGQNGVRANS 290

Db 234 -LQSITTLANLTGPYSIIGLGAIFGGWNITFGQTL-GIAQNAQGVALLGPXAAAGALS 291

Qy 291 SLGSSIGS---SGIGGGYAANLGRASAISVGSLSVPOVAAANQAVTPAARALPLTSLS 345

Db 292 PLAPRGGYIADITPLGGGATGGTARAVIVGSLSVQPGVNAEAPMVRASVLPGTGAP 351

Qy 346 A-AERGPQMLGGLPVGCMGARAGGGSLGVLPYRPMYHPSAAG 377

Db 352 ALAAEAPGALFGEMALSLAGRALAGTAVRSAGAARV 389

Qy 367 TVSAAPEAAGPSLIGGLP---AGAGGAGAGP-RYGFPTVMARPPFG 411

Q99Q11 PRELIMINARY; PRT; 409 AA.

AC Q99Q11; PRELIMINARY; PRT; 409 AA.

DB 01-JUN-1998 (TREMBLrel. 06, Created)

DB 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DE PPE-family protein.

DR MTW049-30.

DR RN 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DR PPE-family protein.

DR Rv1806 OR MTW049-30.

DR Mycobacterium tuberculosis.

OC Corynebacteriaceae; Actinomycetales; Mycobacterium.

OC Bacteria; Actinobacteria; Actinomycetales; Mycobacterium.

OC Corynebacteriaceae; Mycobacterium.

OC NCBI_TaxID=1773;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=H337RV;

RX MEDLINE=98295987; PubMed=9634230;

RX Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Barnham D., Brown D., Chillingworth T., Connor R., Davies R., Devinlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Krogh A., McLean J., Moulie S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squires R.,

Best Local Similarity 42.8%; Pred. No. 3.2e-34; Matches 182; Conservative 60; Mismatches 122; Indels 61; Gaps 13;

QY 2 VDFGALPPRENSARMYAGPGSASLVAACMWDSVASYLSSAASFOSVWGLTVGSIGS 61
 DB 1 MDFATLPPRENSARMYSGGSAPMLAAASAWHGLSAEDRASALSYSSVYSTJGEHWGP 60

QY 62 SAGIMVAAASPYAAMSVTAAQVRAAAYAETAYGLTPPPVIAENRAEMIL 121
 DB 61 ASASNTAAAPYVAAAMSVTAAVRAEQAQAAEAAAAYAFAATPPEVIEANRAQMLN 120

QY 122 IATNLGQNTPAIAVNEAFYGYEMQDAAMFGYAATAATTATLPPFPEADEMTSAGGL 181
 DB 121 IATNLGQQAPATATEAQYAENWSQDAMAMYGAAGASAAT QLTFTEPPTQTTNAASGL 179

QY 182 LEQPLAVEREASDTAA----NOLMANTPQALQQLAQPTQGET--PSSKUG----- 225
 DB 180 AAQSAAIATBASAGAQQTTLISOLIAAAPSVLQGLSSSTAATASAPSGLLGLGSGS 239

QY 226 ---GLWKTVSPHRSPISNNVSMANMHMNTNSGVM-TNTLS---SMIKGFAPAAAQAV 278
 DB 240 WLDXKLWALLDPN-----SNFWNTIASSGLFLPNTIAFPFLGLGGVAAADAGDV 289

QY 279 QTAQONGYRAMSIGSSL----GSSGJICGGVAAANLGRASVGSLSVPOQAWAAANOQAVP 333
 DB 290 LGEATSG----GLGGALVAPLOSSAGGGJGTVAIQLNATGTLSVSPSWTAAPLASP 344

QY 334 AARAL---PLTSLTSAAEKGPGQMGLLGFLPGONGARAGGGLGSVLRVPP---RPYMPH 386
 DB 345 LGSALGGTDMVAPPDAVAG---MPGMFEGTNGQGFG----RAVPQYGRPNFVAR 394

QY 387 SPAAG 391.
 DB 395 PPAAG 399.

RESULT 13
 ID OS31956 PRELIMINARY; PRT; 403 AA.
 AC OS31956;
 DT 01-JUN-1998 [TREMBLrel. 06, Created]
 DT 01-JUN-1998 [TREMBLrel. 06, Last sequence update]
 DT 01-JUN-2003 [TREMBLrel. 24, Last annotation update]
 DE PPE-family protein
 GN RVI1807 OR MT1856 OR MTv049.29.
 OC Mycobacterium tuberculosis.
 Bacteria: Actinobacteria: Actinomycetidae: Actinomycetales:
 NCBI_TaxID=1773;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=I337RV;
 RX MEDLINE=98295387; PubKey=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigleiner K., Gao S., Barry C.E., III, Tekala P.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S.,
 RA Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Barrell B.G.;
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-541(1998).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Hatt D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umeyama L.A., Brimble M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and

RT laboratory strains"; Submitted (APR 2001) to the EMBL/GenBank/DDBJ databases.
 RL DR EMBL; AL012021; CAA17728.1;
 DR DR PIR; H70931; H0931.
 DR DR TIGR; MT1856;
 DR DR InterPro; IPR00030; Microbac_PPE.
 KW DR Complete proteome.
 FT DR PFMam; PF00283; PPE; 1.
 CONFLICT 227 227 F -> S (IN REF. 2).
 FT DR 238 V -> L (IN REF. 2).
 CONFLICT 403 AA; 39243 MW; DCR188804FD15-CBE CRC64;
 SQ DR

Query Match 37.8%; Score 737.5; DB 16; Length 403;
 Best Local Similarity 42.6%; Pred. No. 4.8e-34;
 Matches 181; Conservative 60; Mismatches 123; Indels 61; Gaps 12;

QY 2 VDFGALPPRENSARMYAGPGSASLVAQNMDSVASYLSSSTAATASAPSGLLGLGSGS 61
 DB 5 LDFATLPPRENSARMYSGGSSAPMLAAASAWHGLSAEDRASALSYSSVSLSTLTGEHWGP 64

QY 62 SAGIMVAAASPYAAMSVTAAVRAAAYAETAYGLTPPPVIAENRAELMIL 121
 DB 65 ASASNTAAAPYVAAAMSVTAAVRAEQAQAAEAAAAYEAFAATATPPVIEANPAQLMAL 124

QY 122 IATNLGQNTPAIAVNEAFYGYEMQDAAMFGYAATAATTATLPPFPEADEMTSAGGL 181
 DB 125 IATNLGQNTPAIAVNEAFYGYEMQDAAMFGYAATAATTATLPPFPEADEMTSAGGL 181

QY 162 LEQAAVEEABSDTAA-----NOLMNNYQPAQQLAQOPTGT-----TPSS 222
 DB 184 AAQSAAIATBASAGAQQTTLISOLIAAAPSVLQGLSSSTAATFASGPSLLGTVGSGSS 243

QY 223 KLGGLKTVSPHRSPLISNNMSMANTHMSMTNSGUM-TNTLS---SMIKGFAPAAAQAV 278
 DB 244 WLDKLWALLDPN-----SNFWNTIASSGLFLPNTIAFPFLGLGGVAAADAGDV 293

QY 279 QTAQONGYRAMSIGSSL----GSSGJICGGVAAANLGRASVGSLSVPOQAWAAANOQAVP 333
 DB 294 LGERTSG----GLGGLVALPGLSGGGLGTVAAIQLGNATVGLTSLVSPSWTAAPLASP 348

QY 334 AARAL---PLTSLTSAAEKGPGQMGLLGFLPGONGARAGGGLGSVLRVPP---RFYVMPH 386
 DB 349 LGSALGGTDMVAPPVAAG---MPGMFEGTNGQGFG----RAVFQYGRPNFVAR 398

QY 387 SPAAG 391.
 DB 399 PPAAG 403

RESULT 14
 ID OS31950 PRELIMINARY; PRT; 423 AA.
 AC OS31950;
 DT 01-JUN-1998 [TREMBLrel. 06, Created]
 DT 01-JUN-1998 [TREMBLrel. 06, Last sequence update]
 DT 01-OCT-2003 [TREMBLrel. 25, Last annotation update]
 DB PPE-family protein.
 GN RV1801 OR MTv049.23 OR MT1856.
 OC Mycobacterium tuberculosis.
 OC Bacteria: Actinobacteria: Actinomycetales;
 OC Corynebacterineae: Mycobacteriaceae; Mycobacterium.
 OC NCBITaxID=1773;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=H337RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigleiner K., Gao S., Barry C.E., III, Tekala P.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Barrell B.G.;
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis clinical and

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.J., Rutten S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence"; *Nature* 393:537-544 (1998).

Mycobacterium bovis.
Bacteria; Actinomycetidae; Actinomycetales;
Corynebacteriinae; Mycobacteriaceae; Mycobacterium.

Query Match							
EMBL; AE007044;	Score 736;	DB 16;	Length 423;				
PIR; B70931;	Best Local Similarity 41.83;	Pred. No. 6.2e-34;					
TIGR; MT11850;	Matches 182;	Conservative 50;	Mismatches 123;	Indels 80;	Gaps 12;		
DR							
DR							
DR							
DR							
KW							
Complete proteme.							
InterPro; IPR000030;	Microbac_PPE.						
PFAM; PF00823;	PPE.	1.					
SEQUENCE	443 AA;	41477 MW;	26E52CC271FBBF57	CRC64;			
Query Match	37.8%	Score 736;	DB 16;	Length 423;			
Best Local Similarity	41.8%	Pred. No. 6.2e-34;					
Matches	182;	Conservative	50;	Mismatches 123;	Indels 80;	Gaps 12;	
Qy							
2 VDFGALPPEINSARMYAGPGSASLYAAQWMDVSASDLSASAPPSVWGLTVSSWIGS 61	Db	2 VDFGALPPEINSARMYAGPGSASLYAAQWMDVSASDLSASAPPSVWGLTVSSWIGS 61	Db	1 MDGLLPPBPEINSGRMYTGPGPMPMIAATANDGLAELHATAAGYSELSELT-GAWSGP 59			
2 VDFGALPPEINSARMYAGPGSASLYAAQWMDVSASDLSASAPPSVWGLTVSSWIGS 61	Qy	62 SAGLMVAAASPYAAMSVTAGQAELTAQVRAAAAYETAYGLTVPPVIAENRAELMIL 121	Qy	62 SAGLMVAAASPYAAMSVTAGQAELTAQVRAAAAYETAYGLTVPPVIAENRAELMIL 121	Db	60 SSTNSMASAAPYAMSVTAGQAELTAQVRAAAAYETAYGLTVPPVIAENRAELMIL 119	
1 MDGLLPPBPEINSGRMYTGPGPMPMIAATANDGLAELHATAAGYSELSELT-GAWSGP 59	Db	60 SSTNSMASAAPYAMSVTAGQAELTAQVRAAAAYETAYGLTVPPVIAENRAELMIL 119	Db	122 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Qy	122 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Db
60 SSTNSMASAAPYAMSVTAGQAELTAQVRAAAAYETAYGLTVPPVIAENRAELMIL 119	Qy	120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Qy	120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Db	120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Qy
62 SAGLMVAAASPYAAMSVTAGQAELTAQVRAAAAYETAYGLTVPPVIAENRAELMIL 121	Db	120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Qy	120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Db	120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Qy
122 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 181	Qy	122 SKLGGIWKTSVPHRSPISPNMSMANTHMSMTNSGVSMTNTLSSMLRGFAAAAAQAVTA 281	Qy	122 SKLGGIWKTSVPHRSPISPNMSMANTHMSMTNSGVSMTNTLSSMLRGFAAAAAQAVTA 281	Db	122 SKLGGIWKTSVPHRSPISPNMSMANTHMSMTNSGVSMTNTLSSMLRGFAAAAAQAVTA 281	Qy
120 IATNLGQNTTAAIAVNEAIGEMWAQDAAMFGYAATAATAATATLPPFEEAPEMTSAGGL 178	Db	123 9 TFLGG--AVTGPyTFFP-----GVLPSPGVYLLGIQSVL-----v 271	Db	123 9 TFLGG--AVTGPyTFFP-----GVLPSPGVYLLGIQSVL-----v 271	Qy	123 9 TFLGG--AVTGPyTFFP-----GVLPSPGVYLLGIQSVL-----v 271	Db
182 LEQAAVEDESDTAAN-----QLMNNVPQALQLAQPT----QGTTP-----S 221	Qy	128 2 AQNGVYRAMSSUGS-----SIGSSGIGGG-VAAANGLRAASVGSL-----S 319	Qy	128 2 AQNGVYRAMSSUGS-----SIGSSGIGGG-VAAANGLRAASVGSL-----S 319	Db	128 2 AQNGVYRAMSSUGS-----SIGSSGIGGG-VAAANGLRAASVGSL-----S 319	Qy
179 GAQSSAAQTTAAAGGNLQSAPPQLSAVRALQGLALPTASQCSASATPQWVTDGLNLS 238	Db	127 2 TONGQGSALLKGKGPITGALAPLAEFAHTPLIPGSEGGGSVAGIGRAGIVGKLS 331	Qy	127 2 TONGQGSALLKGKGPITGALAPLAEFAHTPLIPGSEGGGSVAGIGRAGIVGKLS 331	Db	127 2 TONGQGSALLKGKGPITGALAPLAEFAHTPLIPGSEGGGSVAGIGRAGIVGKLS 331	Qy
222 SKLGGIWKTSVPHRSPISPNMSMANTHMSMTNSGVSMTNTLSSMLRGFAAAAAQAVTA 281	Qy	130 2 VPOQWAIAANQAVTPAARALPLTSLS--AAERGPQGMGLPVQMGARAGGGLSGVLR 376	Qy	130 2 VPOQWAIAANQAVTPAARALPLTSLS--AAERGPQGMGLPVQMGARAGGGLSGVLR 376	Db	130 2 VPOQWAIAANQAVTPAARALPLTSLS--AAERGPQGMGLPVQMGARAGGGLSGVLR 376	Qy
239 TFLGG--AVTGPyTFFP-----GVLPSPGVYLLGIQSVL-----v 271	Db	132 2 VPOQWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Qy	132 2 VPOQWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Db	132 2 VPOQWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Qy
282 AONGVRAMS SLGS-----	Qy	137 2 VPPRPyTMMPHSPAAAG 391	Qy	137 2 VPPRPyTMMPHSPAAAG 391	Db	137 2 VPPRPyTMMPHSPAAAG 391	Qy
272 TONGQGSALLKGKGPITGALAPLAEFAHTPLIPGSEGGGSVAGIGRAGIVGKLS 331	Qy	138 2 -HPQSAAPAVG 400	Qy	138 2 -HPQSAAPAVG 400	Db	138 2 -HPQSAAPAVG 400	Qy
320 VPOQWAIAANQAVTPAARALPLTSLS--AAERGPQGMGLPVQMGARAGGGLSGVLR 376	Db	139 2 VPOQWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Qy	139 2 VPOQWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Db	139 2 VPOQWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Qy
332 VPQGWTVAAPETPSPPAALQATRILAAPIATADGCAALGOMALSCLAGRAAAGSTG--- 388	Db						

2Y 377 VPPRPyNMHSPAG 391
DD 389 -- HPIGSAAAPAVG 400

RESULT 15

Q7TZA4 PRELIMINARY; PRT; 423 AA.
AC Q7TZA4;
DT 01-OCT-2003 (TREMBrel. 25, Created)
DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
DI 01-OCT-2003 (TREMBrel. 25, Last annotation update)
PPE family p
PPEB29 OR MB1829.

Scoring table:	BLOSUM62				
Gapop 10.0 , Gapext 0.5					
Searched:	141681 seqs, 52070155 residues				
Total number of hits satisfying chosen parameters:	141681				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing First 45 summaries				
Database :	SwissProt_42:*				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
-	-	-	-	-	-
1	1656.5	85.0	396	1 YD61_MYCTU	Q11031 mycobacteri
2	705	36.2	408	1 YS92_MYCTU	Q10813 mycobacteri
3	688	35.3	463	1 Y102_MYCTU	Q13951 mycobacteri
4	444	22.8	487	1 Y442_MYCTU	P42611 mycobacteri
5	426	21.9	443	1 YB78_MYCTU	Q10540 mycobacteri
6	418	21.4	678	1 YF48_MYCTU	Q10778 mycobacteri
7	364.5	18.7	408	1 SRA_MYCLE	Q07297 mycobacteri
8	324.5	16.6	463	1 Y096_MYCTU	Q10892 mycobacteri
9	324	16.6	434	1 YU18_MYCTU	P31500 mycobacteri
10	321.5	16.5	435	1 YU21_MYCTU	Q33268 mycobacteri
11	323.5	12.0	178	1 YY29_MYCTU	P06246 mycobacteri
12	217	11.2	176	1 YY25_MYCTU	Q50703 mycobacteri
13	153.5	7.9	860	1 ELS_MOUSE	P54220 mus musculus
14	151.5	7.8	232	1 YY26_MYCTU	Q50702 mycobacteri
15	150	7.7	864	1 ELS_BAR	Q39372 rattus norvegicus
16	143.5	7.4	730	1 ELS_HUMAN	P15502 homo sapiens
17	139.5	7.2	881	1 PRY3 YEAST	P47033 saccharomyces cerevisiae
18	135	6.9	907	1 A180_HUMAN	P05041 homo sapiens
19	133.5	6.8	825	1 TCP0_HSV2A	P28284 herpes simplex virus type 2
20	133.5	6.8	2432	1 Y43R_IRV6	P18305 chilo iridovirus
21	132	6.8	1120	1 STFR_ECOLI	P76072 escherichia coli
22	132	6.8	2090	1 N214_HUMAN	P35658 homo sapiens
23	131	6.7	836	1 VG26_BPM15	Q01233 mycobacteri
24	131	6.7	1150	1 APMU_PIG	P20221 sus scrofa
25	129	6.6	1783	1 RAA3_CHLRE	Q9fec4 chlamydomonas
26	128	6.6	779	1 SRP_DROME	P52172 drosophila melanogaster
27	127.5	6.5	790	1 ANP_NOTOCO	P24856 notothenia
28	126	6.5	354	1 YAU_SCHPO	Q10169 schizosaccharomyces pombe
29	125.5	6.4	1211	1 BUN2_DROME	P24523 drosophila
30	125	6.4	577	1 CST2_HUMAN	P33240 homo sapiens
31	124	6.4	2090	1 HFC1_MESEAU	P51611 mesocricetus auratus
32	123.5	6.3	677	1 Y36_MYCTU	P350597 mycobacteri
33	123	6.3	432	1 YF10_MYCTU	P71789 mycobacteri

ALIGNMENTS

RESULT 1
 YD61_MYCTU STANDARD; PRT; 396 AA.
 ID YD61_MYCTU
 AC Q11031; DT 01-OCT-1996 (Rel. 34, Created)
 AC Q10813; DT 01-OCT-1996 (Rel. 34, Last sequence update)
 AC Q13951; DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB HYPOTHETICAL PROTEIN FAMILY PROTEIN RV1361C/MT1406.
 GN RV1351C OR MT1406 OR MYCTU2B10_25C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TAXID=1773;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H313RV;
 RX PMID=98195987; PubMed=9634230;
 RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmüller K., Gas S., Barry C.E., III, Tekla F., Connor R., Badcock K., Batham D., Brown D., Chillingworth T., Holroyd S., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence"; RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494 / PubMed=112218036;
 RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.F., DeBoy R., Gwinn M., Haft D., Hickie E., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M., RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains." / RL International 184:547-549 (2002).
 CC - SIMILARITY: Belongs to the mycobacterial PPE family.

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 CC DR EMBL; Z75555; CA998166.1; -.
 CC DR EMBL; AE007013; AA9K45669.1; -.
 CC DR PIR; H70741; H70741.
 CC DR TIGR; MT1406; -.
 CC DR Tuberculist; RV1361C; -.
 CC DR InterPro; IPR00030; Microbac_PPE.

SQ	SEQUENCE	463 AA;	463 AA;	46021 MW;	EE64828BF09FA551 CRC64;
RESULT 3					
Y102 MYCTU STANDARD; ID: 053951;	PRT: 463 AA.				
AC DT 30-MAY-2000 (Rel. 39, Created)					
DT 30-MAY-2000 (Rel. 39, Last sequence update)					
DT 10-OCT-2003 (Rel. 42, Last annotation update)					
DB Hypothetical PPE-family protein Rv1802/Mtb1830.					
OS Mycobacterium tuberculosis, and					
OS Mycobacterium bovis.					
OC Bacteria; Actinobacteria; Actinomycetales;					
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.					
OX NCBI_TaxID:1773, 1765;					
RN [1]					
SEQUENCE FROM N.A.					
SPECIES M_tuberculosis; STRAIN=H37Rv;					
PC MEDLINE=19825937; PubMed=9634230;					
RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Barry C.E., III, Tekla P., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;					
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544 (1998).					
RN [2]					
SEQUENCE FROM N.A.					
SPECIES M_tuberculosis; STRAIN=CDC 1551 / Oshkosh;					
RC MEDLINE=222056494; PubMed=12218016;					
RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwin M., Hatt D., Hickey E., Kolonay J.F., Nelson W.C., Umeyama L.A., Brimley M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.;					
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).					
RN [3]					
RP SEQUENCE FROM N.A.					
RC SPECIES M_bovis; STRAIN=AF2122/97;					
RX MEDLINE=22703107; PubMed=12188972;					
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Peterson J., DeBoy R., Dodson R., Gwin M., Hatt D., Hickey E., Kolonay J.F., Nelson W.C., Umeyama L.A., Brimley M., Salzberg S.L., Harris B., Atkin R., Grondin S., Lacroix C., Monsenje C., Simon S., Duthoy S., Grondin S., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Atkin R., Doggett J., Mayes R., Gordor S.V., Hewinson R.G.;					
RT "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).					
CC -!- SIMILARITY: Belongs to the mycobacterial PPE family.					
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CC EMBL; AL022021; CAA1773.1; AB007044; AXK46123.1; BB248349; CAD94533.1; PIR; C70931; C70931.					
CC TIGR; MTB1851; -.					
CC InterPro; IPR00030; PPE; 1.					
CC Hypothetical protein; Complete proteome proteo;					
FT CONFLICT 401 -> L (IN REF. 2).					
RN SEQUENCE FROM N.A.					
RC STRAIN=CDC 1551 / Oshkosh;					
RESULT 4					
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DB NSMLGIGFEAESKMYLPANDIVISTIFGMQFQKPFNPVFPNPDLIPK;					
QY 239 -----SNMYSMANHMSMTNSGVSMNTLSSMLKGFAPAAAQAVOTAAGNGYRA					
QY 182 LEQALAEVEASDAAQNLMNVPQALQOQAPQTGTTESSKLGLWTVS--PHRSPL-					
Db 179 ATQGYVAQANGASAGN-ARSLVSEVLBLLA-TAGTNTVNKTVASLMLNAVTGPYASSV					
QY 236 NSMLGIGFEAESKMYLPANDIVISTIFGMQFQKPFNPVFPNPDLIPK-----					
QY 289 MSSLGSIG----SSGLGG----GVAANLGRAASVGSLSYPOAWAANQAVTAATPAARALPL					
QY 284 -SALGPGLGLRSATSSGLGSTAPASAGSQAGSQQAGSMVPPSAATAATPAIRTYAAVFS					
Qy 341 TSLTS--AAERGPQGML-----GLPVGOMGARAGGGLSGYLRV					
Qy 343 TGLQAVWPAAANISEGSLSQMALASVAGGAAARATGFLGGCRV					
Db 343 TGLQAVWPAAANISEGSLSQMALASVAGGAAARATGFLGGCRV					
RN [3]					
RP SEQUENCE FROM N.A.					
RC SPECIES M_tuberculosis; STRAIN=CDC 1551 / Oshkosh;					
RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwin M., Hatt D., Hickey E., Kolonay J.F., Nelson W.C., Umeyama L.A., Brimley M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.;					
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).					
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CC EMBL; AL022021; CAA1773.1; AB007044; AXK46123.1; BB248349; CAD94533.1; PIR; C70931; C70931.					
CC TIGR; MTB1851; -.					
CC InterPro; IPR00030; PPE; 1.					
CC Hypothetical protein; Complete proteome proteo;					
FT CONFLICT 401 -> L (IN REF. 2).					
RN SEQUENCE FROM N.A.					
RC STRAIN=CDC 1551 / Oshkosh;					
RESULT 5					
Y442 MYCTU STANDARD; ID: Y442 MYCTU STANDARD; AC P42611; DT 01-NOV-1995 (Ref. 32, Created) DT 16-OCT-2001 (Ref. 40, Last sequence update)					
DB Hypothetical PPE-family protein Rv0442c/Mt0458.					
GN RN					
OS Mycobacterium tuberculosis.					
OC Bacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacterium; Corynebacteriales; Mycobacterium.					
OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium.					
OC Corynebacteriales; Mycobacterium; Corynebacteriinae; Mycobacterium.					
OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium.					
OC Corynebacteriales; Mycobacterium; Corynebacteriinae; Mycobacterium.					
OC Corynebacteriales; Mycobacterium; Corynebacteriinae; Mycobacterium.					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=H37Rv;					
RA SEQUENCE FROM N.A.					
RA MEDLINE=93295987; PubMed=9634230;					
RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eggleman K., Gas S., Barry C.E., III, Tekla P., Badcock K., Bahraini K., Brown D., Chillingworth T., Connor R., Davies R., Devin K., Feltwell T., Gentle S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Seeger K., Skelton S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;					
RA Shinick T.M.; RT "The 65-kilodalton antigen of Mycobacterium tuberculosis."; J. Bacteriol. 169:1080-1088 (1987).					
RA RN					
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RA MEDLINE=93295987; PubMed=9634230;					
RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eggleman K., Gas S., Barry C.E., III, Tekla P., Badcock K., Bahraini K., Brown D., Chillingworth T., Connor R., Davies R., Devin K., Feltwell T., Gentle S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Seeger K., Skelton S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;					
RA Shinick T.M.; RT "The 65-kilodalton antigen of Mycobacterium tuberculosis."; J. Bacteriol. 169:1080-1088 (1987).					
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RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eggleman K., Gas S., Barry C.E., III, Tekla P., Badcock K., Bahraini K., Brown D., Chillingworth T., Connor R., Davies R., Devin K., Feltwell T., Gentle S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Seeger K., Skelton S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;					
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RA Shinick T.M.; RT "The 65-kilodalton antigen of Mycobacterium tuberculosis."; J. Bacteriol. 169:1080-1088 (1987).					
RA RN					
RA SEQUENCE FROM N.A.	</				

RX	Medline:22206494; PubMed:12218036;
RA	Fleischmann R.D., Alland D., Baisen J.A., Carpenter L., White C.,
RA	Gwynn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Brmoaeva M., Salzberg S.L., Utterback T., Weidman J., Khouri H., Gill J., Nikula A., DeJager A., Utterback T., Weidman J., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.; "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; J. Bacteriol. 184:5479-5490 (2002).
CC	- - SIMILARITY: Belongs to the mycobacterial PPE family.
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CC	EMBL; M15467; AAAB825.1; ALT_INIT.
DR	EMBL; AL021532; CAA1399_1; -.
DR	EMBL; AE0005948; AAK14681_1; -.
DR	PIR; C70830; C70830.
DR	TIGR; MT0451; -.
DR	TubercuList; Rv0442C; -.
DR	InterPro; IPR000330; Microbac_PPE.
DR	InterPro; IPR00989; Mycobac_Pentapep.
DR	Pfam; PF01669; Pentapeptide_2; 5.
DR	Pfam; PF00823; PPE_1.
KW	Hypothetical protein; Complete proteome.
FT	CONFLICT .40 40 E -> K (IN REF. 2).
FT	CONFLICT .96 96 I -> T (IN REF. 1).
FT	CONFLICT .211 211 G -> GRNNIG (IN REF. 1).
SQ	SEQUENCE 487 AA; 47247 MW; 97224D5B16C8C7F CRC64;
Query Match	22.8%; Score 444; DB 1; Length 487;
Best Local Similarity	32.1%; Pred. No. 4-8e-19;
Matches 135;	Conservative 48; Mismatches 180; Indels 58; Gaps 12;
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Db	6 FAWLPPEINSALMFGPGSPGLIAATTAQGBLAETLASASLGSTSETSGANLGPSSA
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Qy	229 KTVS-----PHRSPISNVNMSMANNHSMTNMSMNTLSSMLKGFPAPAAAQAYQ
Db	288 GSGNTIGNSLNSLNSIGTSCT---INAGIG---SAGSNT-SPNAGNQNAAGSAAAGS
Qy	340 LTSLTSAERPGQM---LGGLPVQMGARAG--GGISGVLR -VPPRPYVMHSPPSA
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Qy	391 G 391
Db	401 G 401

Y878	MYCTU		
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AC	Q10540; Q10540; Q10540;		
DT	01-OCT-1986 (Rel. 34, Created)		
DT	01-OCT-1986 (Rel. 34, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Hypothetical PBP-family protein Rv078ac/MTO901.		
GN	Rv078ac OR MTO901 OR MTCY31.06C.		
OS	Mycobacterium tuberculosis.		
OC	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;		
OX	Corynebacteriales; Mycobacteriaceae; Mycobacterium.		
RN	NCBI_TaxID=1773;		
[1]			
RP	SEQUENCE FROM N.A.		
RC	STRAIN=H7Rv;		
RX	MEDLINE=98295987; PubMed=9634230;		
RA	Gordon S.V., Bigmiller K., Gas J.J., Garnier T., Churcher C., H.		
RA	Colle S.T., Brosch R., Parkhill J., Barry C.E. III, Tekala F.,		
RA	Connor R., Connor D., Chillingworth T., Connor R.,		
RA	Badcock K., Basham D., Brown D., Gentles S., Hamlin N., Hol		
RA	Davies R., Devilin K., Feltwell T., Gentleman J., Hamlin N., Murphy		
RA	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Rogers J.,		
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,		
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,		
RA	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;		
RT	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";		
RL	Nature 393:537-544 (1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CDC 1551 / Oshkosh;		
RX	MEDLINE=12204949; PubMed=12218016;		
RA	Fleischmann R.D., Allard D., Eiser J.A., Carpenter L., White		
RA	Peterson J.J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickie E.,		
RA	Kolenow J.F., Nelson W.C., Umayam L.A., Salzberg S.,		
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mik		
RA	Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;		
RT	"Whole-genome comparison of Mycobacterium tuberculosis clinic		
RT	laboratory strains";		
RL	J. Bacteriol. 184:5479-5490 (2002).		
CC	-- SUBCELLULAR LOCATION: Integral membrane protein (Potential		
CC	-- SIMILARITY: Belongs to the mycobacterial PPE family.		
CC	This SWISS-PROT entry is copyright. It is produced through a		
CC	between the Swiss Institute of Bioinformatics and the EMBL		
CC	the European Bioinformatics Institute. There are no restrictions		
CC	use by non-profit institutions as long as its content is		
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CC	entities requires a license agreement (See http://www.isb-sib.ch)		
CC	or send an email to license@isb-sib.ch .		
DR	EMBL; Z23101; CAA97383/1; -; ALT_INIT.		
DR	PIR; C70780; C70780.		
DR	TIGR; MT0901; -.		
DR	Tubercolist; Rv078ac; -.		
DR	InterPro; IPR000030; Microbac PPE.		
DR	InterPro; IPR002989; Mycobac_Pentapep.		
PFam	PF001469; Pentapeptide_2; 4.		
DR	PFam; PF00823; PPE_1.		
KW	Hypothetical protein; Transmembrane; Repeat; Complete proteom		
PT	TRANSMEM 15 35 POTENTIAL.		
PT	TRANSMEM 38 38 POTENTIAL.		
PT	TRANSMEM 59 79 POTENTIAL.		
PT	TRANSMEM 181 201 POTENTIAL.		
PT	DOMAIN 64 73 POLY-ALA.		
PT	DOMAIN 81 115 ALA-RICH.		
PT	DOMAIN 231 270 4 X 10 AA APPROXIMATE REPEATS.		
SQ	SEQUENCE 443 AA; 43592 MW; C58BSC607F0675B2 CRC64;		
SQ	SEQUENCE 443 AA; 43592 MW; C58BSC607F0675B2 CRC64;		

2	VDFGALPPEBINSARMYAGPGSASLVAARQMDVSADLSSAASFQSYVWGIUTVG---SW	58
1	MNFMVLPPBEVNSARIVAGAPMLAAVADGLAELGMAMASFLSLISGTAGPSAW	60
59	IGSSAGIMVAASPYVWMSVTAGOELTAQVRAAAAYETAYGLTVPPVIAENRAEL	118
61	QFGEAAAAPYLSSWLNAATIARAEGAAAGKAAAAYEARAAATAHPALVAANRNQL	120
119	MILIATNLILGONTPAIAYNEAEYGEMNAQDRAAMEFGYAAATATATATLIPFEPEAPNTSA	178
121	LSQLVLSNLIFGNQNPAAATEASYEQLWADQVAMVGTHGGASTVASQITPWQQ-----	173
Db	DR InterPro: IPR000030; Microbac PPE.	
Db	DR InterPro: IPR002989; Mycobac PPE.	
Db	DR InterPro: IPR002989; Pentapep.	
Db	DR Pfam: PF01469; Pentapeptide_2;	11.
Db	DR PPE: PPE_1.	
Db	KW Hypothetical protein; Transmembrane; Complete proteome.	
Db	KW TRANSMEM 14	34
Db	FT TRANSMEM 180	200
Db	FT CONFLICT 258	258
Db	SEQUENCE 678 AA;	67636 MW;
Db	Query Match 21.4 %; Score 418; DB 1; Length 678;	
Db	Best Local Similarity 31.9 %; Pred. No. 2. Pre-17;	
Db	Matches 106; Conservative 48; Mismatches 140; Indels 38; Gaps 7;	
Db	Qy 2 VDFGALPPEBINSARYAGPGSASLYAAQOMWDVSAYSDLPSAASAFOQSYVWGLTVESWIGS	61
Db	Db 1 MNFSVLPPEINSALMFAAGCPGPMAAASAWTGLADLGAAASASAVTSQLATSSWQGP	60
Db	Qy 62 SAGLMVAAASPYVWMSVTAGQELTTAQYRVAAYAETAYGLTVPPVIAENRAEL	121
Db	Db 61 ASAATMGVAAASYARVLTAAAQEOAAGQAOAAVSFAEEAALAAATTPGAVSANGGRLRS	120
Db	Qy 122 IATNLIGONTPAIAYNEAEYGEMNAQDRAAMEFGYAAATATATLIPFEPEAPNTSA	180
Db	Db 121 VASNLLQGNQAPAIAYVEAVYEQMWAAVDAAMLGTVGEASAVALSITPFTPSAATPTGG	180
Db	Qy 181 -----LLEQQAAVEEASDAAANQMLNNVPOALQLOQOPTGTTPSSKLGLGMKTVS	232
Db	Db 181 AVIIAGFPFDLGNVTTGGNLLASGNLGLGNLGS-----FNGSANTGSVNLN-----	229
Db	Qy 233 PHRSPTSNM-VSMANNHMMTNCSYMTNTLMSLKGFAAAAQAVQTAQONGYRAMS	290
Db	Db 230 -----ANTGPLNLGGNIGSYNLLGNGNQDNLN-----PDSGNITGLNWGSQNGSYN	276
RESULT 6		
YP48_MYCTU	STANDARD; PRT; 678 AA.	
AC	AC YF48_MYCTU	
DT	DT Q10778; (Rel. 34, Created)	
DT	DT 01-OCT-1996 (Rel. 38, Last sequence update)	
DT	DT 15-JUL-1999 (Rel. 42, Last annotation update)	
DT	DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DE	DE Hypothetical PPE-family Protein Rv1548c/MT1599.	
GN	GN Rv1548C OR MT1599 OR MTcY48.17.	
OS	OS Mycobacterium tuberculosis.	
CC	CC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Mycobacterium.	
OC	OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
NCBI_TaxID	NCBI_TaxID:1773;	
RN	RN SEQUENCE FROM N.A.	
RP	RP STRAIN=H37RV;	
RX	RX MEDLINE=9829987; PubMed=9634230;	
RA	RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Telkai E., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B. G.;	
RA	RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence." Nature 39:537-544(1998).	
RT	RT	
RL	RL SEQUENCE FROM N.A.	
RP	RP STRAIN=CDC 1551 / Oshkosh;	
RX	RX MEDLINE=2206494; PubMed=12218036;	
RA	RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Utley W.A., Ermoljeva M., Salzberg S.L., Delcher A., Utterback R., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;	
RA	RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; J. Bacteriol. 184:5479-5490(2002).	
RT	RT - SIMILARITY: Belongs to the mycobacterial PPE family.	
RL	RL SEQUENCE FROM N.A.	
RP	RP Bacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
OC	OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
OX	OX NCBI_TaxID:1769;	
RN	RN SEQUENCE FROM N.A.	
RP	RP MEDLINE=9343922; PubMed=9478104;	
RA	RA Vega-Lopez F., Brooks L.A., Dockrell H.M., de Smet K.A.L., Thompson J.K., Hussain R., Stoker N.G.;	
RA	RA "Sequence and immunological characterization of a serine-rich antigen from Mycobacterium leprae"; Infect. Immun. 61:2145-2153(1993).	
RT	RT	
CC	CC [2] SEQUENCE FROM N.A.	
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EPFL, on instruction -	

RX MEDLINE=91020554; PubMed=7934845;	QY 214 ---PQQ-----GTPSSKLGGIWKVTKVSPHRSPIANNVSMANNHMSMTNSGVMTNT 261
RA Rinke de Wit T.P., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,	DR 240 PFGTPSSQSNLDSATSLTQQLGSU-----DTSIASSLTTNS--ISSST 286
RA Jonsen A.A.M., Thole J.E.R.,	DR 262 LSSMLKGAFAPAAAQVQTAQAQNGVRAAQSGLGGVAA----LGRAASVG 316
RT "A Mycobacterium leprae-specific gene encoding an immunologically	DR 287 ASSIM---PIVASQVTETGRSQV-AVEKMQISSTAVSVDVAASSKVAGVQAVSVG 341
RT recognized 45 kDa protein."	DR 317 SLSVPQAWIAANAOVATPAAPALP-LTSLTSAERGPQGMGLGGHPVGQMGARAGGGIISGV 374
RL Mol. Microbiol. 10:829-838 (1993).	DR 342 ALRVPPENWATASQPVMATAHSVPAGCSAITA-----VSGPLBGV 381
RN [3]	
RP SEQUENCE FROM N.A.	
RC STRAIN=IN;	
RX MEDLINE=1128732; PubMed=11234002;	QY 317 SLSVPQAWIAANAOVATPAAPALP-LTSLTSAERGPQGMGLGGHPVGQMGARAGGGIISGV 374
RA Cole S.T., Eigmeyer K., Parkhill J., James K.D., Thomson N.R.,	DR 342 ALRVPPENWATASQPVMATAHSVPAGCSAITA-----VSGPLBGV 381
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,	
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,	
RA Davies R.M., Devlin K., Dutchoy S., Fraser A., Hamlin N.,	
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., MacLean J., Moule S.,	
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,	
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,	
RA Squares S., Stevens K., Taylor K., Whittlehead S., Woodward J.R.,	
RA Barrell B.G.,	
RT "Massive gene decay in the leprosy bacillus.";	
RL Nature 409:1007-1011(2001).	
CC :- SIMILARITY: Belongs to the mycobacterial PPE family.	
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
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CC or send an email to license@isb-sib.ch).	
CC	
DR U0015; AAC3220_1; -.	Y096 MYCTU STANDARD; PRT; 463 AA.
DR X68431; CAA8480_1; -.	ID Y096 MYCTU STANDARD; PRT; 463 AA.
DR 221952; CAA79950_1; -.	AC Q10832;
DR 257179; CAB0938_1; -.	DR 01-OCT-1996 (Rel. 34, Created)
DR ALB83948; CAC29919_1; -.	DR 01-OCT-1996 (Rel. 34, Last sequence update)
DR P71; C86960; C86960.	DR 10-OCT-2003 (Rel. 42, Last annotation update)
DR PIR; S33522; S33522.	RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
DR PIR; S39872; S39872.	RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
DR Lepronra; ML0411; -.	RA Gordon S.V., Eigmeyer K., Gas D., Hornsby T., Jagels K., Krogh A., McLean J., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
DR InterPro; IPR000030; Microbac_PPE.	RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
DR Pf0022; PPE; 1.	RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
KW Antigen; Repeat; Complete proteome.	RT "Deciphering the biology of Mycobacterium tuberculosis from the
FT DOMAIN 192 196 POLY-SEP.	RT complete genome sequence.";
FT DOMAIN 209 235 2 X 6 AA REPEATS OF S-V-A-Q-S-E.	RN [1]
FT REPEAT 209 235 2 X 6 AA REPEATS OF S-V-A-Q-S-E.	RP SEQUENCE FROM N.A.
FT REPEAT 209 235 2 X 6 AA REPEATS OF S-V-A-Q-S-E.	RC STRAIN=CDC 1551 / Oshkosh;
FT REPEAT 209 235 2 X 6 AA REPEATS OF S-V-A-Q-S-E.	RX MEDLINE=22206194; PubMed=12218036;
FT CONFLICT 132 132 T -> S (IN REF. 2).	RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
FT CONFLICT 189 189 S -> L (IN REF. 2).	RA Peterson J., DeBoy R., Dodson R., Gwin M., Hatt D., Hickey E.,
FT CONFLICT 191 191 H -> D (IN REF. 2).	RA Kolonay J.F., Nelson W.C., Umayam L.A., Bermudeva M., Salzberg S.L.,
FT CONFLICT 292 292 P -> L (IN REF. 2).	RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
SQ SEQUENCE 408 AA; 42466 MW; 5C0CBEB0D6A98 CRC64;	RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.,
Query Match 18.7%; Score 364.5%; DB 1;	RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
Best Local Similarity 26.3%; Pred. No. 1.7e-4;	RT laboratory strains.";
Matches 115; Conservative 72; Mismatches 163; Indels 87; Gaps 11;	RL Bacteriol. 184:5479-5490 (2002).
QY 1 MDFGALPEINSARMYAGPGSASILVAAQWQWDVSADLFASASAFAFQSVVVGLTVGSWIG 60	CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
Db 1 MFDPMVMSPEVNAFLMRSRGPSTPLNGAAEWAWISLAEQLMMAAQEVSDTIWVAPASFAG 60	CC -! SIMILARITY: Belongs to the mycobacterial PPE family.
QY 61 SSAGLMVAAASPVAMSVTAQEAQVRAAAYETGYLTVPPPTAENFAELMI 120	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
Db 61 EISDMLASRSTFVAWLGNAAENAGLIAVRLHAYAAFEERAGMYPLTLGNLIHTMA 120	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
QY 121 LIATNLQGQNTPAIAYNEAKEYGEMWAQDAAMFQIAAATATAATLPPBEAPENTSAGG 180	CC the European Bioinformatics Institute. There are no restrictions on its
Db 121 LIAINWQGQSTIVTAALENDLMMQNSTMATITRDVIRETGMEVNEDAPQVSRY 179	CC use by non-profit institutions as long as its content is in no way
QY 181 LLEQAAAEVEAEDTAANQMNKNVPAQOLQQAQ----- 213	CC modified and this statement is not removed. Usage by and for commercial
Db 180 CMRRDSVNSFHSSSSDLSLIESIDNLYSDVAQSEBBGDSMSQSINTCGSSVAQSELCD5 239	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
	CC or send an email to license@isb-sib.ch).
	CC
	DR EMBL: 274410; CA98932; 1;
	DR EMBL: AE006932; FAK44327; 1;
	DR PIR: H70750;
	DR TIGR: MT0105;
	DR Tuberculist: Rv0096; -.

Nature 393:537-544 (1998).
 [2] SEQUENCE FROM N.A. STRAIN=CDC 1551 / Oshkosh
 MEDLINE=22206434; PubMed=
 Fleissmann R.C., Allard
 Petersson J., DeBoy R., Do
 Kolonay J.F., Nelson W.C.
 Utterback A., Delcher L., Bishai W., Jacobs W.R. Jr
 "Whole-genome comparison
 of bacterial strains." J. Bacteriol. 184:5479-54
 [3] SEQUENCE OF 160-374 FROM
 STRAIN=isolate 50410;
 Patki A.H., Dale J.W.;
 Submitted (APR-1991) to t
 -|- SIMILARITY: Belongs to
 -|- CAUTION: In strain Os
 interrupted in position
 -|- CAUTION: Was original
 -|- CAUTION: Ref 3 sequence
 in positions 294; 337-
 -|- This SWISS-PROT entry is
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 the European Bioinformatics
 use by non profit insti
 modified and this statement
 entities requires a lices
 or send an email to lices
 EMBL; AL0021267; CAA16103
 EMBL; AB007129; AAK41427
 EMBL; AB007129; AAK41430
 EMBL; X92917; CAA41951.1
 PIR; E70857; E70857.
 TIGR; MT31098; -
 TIGR; MT3101; -
 Tuberculous; Rx3018C; -
 InterPro; IP000030; Micc
 Pfam; PF00822; PPB; 1.
 Hypothetical protein; Con
 SEQUENCE 434 AA; 43022
 query Match 16.
 best Local Similarity 28.
 matches 115; Conservative
 6 ALPPINPSARMYAGP
 8 ASPSPVHSALLSGP
 66 MVAAPSPVYAMWVT
 68 FVAAVPVYAWLQQA
 126 LLGONTPAVNEAE
 128 FFGNTTIPALNEAD
 186 AAVEEASDAAAN-
 182 -ANASNAAYAAATTI
 235 ---RSPISNNVSMAN
 238 ILGFNIIIGFPTTLAS
 271 -----PAAAQAOVQ

Db	298 CGPLIGLALAAGVPGVAGLAGVAGLAAL-PAVGAA--AGAPAAVLGVSYAPVSGGVVSPQA	354	Query Match Score 321.5; DB 1; Length 435;
QY	324 WAANGAVTAAPARALPLTSATSAERGPGGMLGGPLPGONGARAGGGILSGV	374	Best Local Similarity 26.5%; Pred. No. 5.6e-12; Matches 53; Mismatches 159; Indels 107; Gaps 12;
Db	355 RLVS -AVEAAPASTSVSUL -ASDRGAZL -GP-VTAGKRSVQFAGI	398	RESULT 10
YU21_MYCTU	YU21_MYCTU STANDARD; PRT; 435 AA.		
ID	053268; 053269;		
AC	053268;		
DT	16-OCT-2001 (Ref. 40, Created)		
DT	16-OCT-2001 (Ref. 40, Last sequence update)		
DT	10-OCT-2003 (Ref. 42, Last annotation update)		
DE	Hypothetical PPE-family protein Rv3021c/Rv3022c/MT3106.		
GN	RV3021c/RV3022c OR MT3106 OR MTv012.35C/MTv012.36C.		
OS	Mycobacterium tuberculosis.		
OC	Bacteria; Actinobacteria; Actinomycetales;		
OC	Corynebacteriae; Mycobacteriaceae; Mycobacterium.		
OX	NCB_TaxID=1773;		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=H7Rv;		
RX	Medline=96295987; PubMed=9644230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Bigmeier K., Gas S., Barry C.E. III, Tekata F., Badcock R., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Skelton S., Squares S., Rogers J., Rutter S., Seeger K., Taylor J.E., Whitehead S., Barrell B.G.; Sulston J.E., Taylor K., Whitehead S., Barrell S., Barrell B.G.; RT		
RT	complete genome sequence."; Nature 393:537-544(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CDC 1551 / Oshkosh;		
RX	Medline=2206494; PubMed=12218036; Fleischmann R.D., Alland D., Eileen J.A., Carpenter L., White C., Kolonay J.F., Nelson W.C., Umayam L.A., Brzuska M., Salzberg S.L., Deicher A., Utterback T., Weidman J.J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; Bacteriol. 184:5479-5490(2002).		
RT	CC :-- SIMILARITY: Belongs to the mycobacterial PPE family.		
CC	-- CAUTION: Ref.1 sequence differs from that shown due to a framework in position 82.		
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DR	EMBL; AL021287; CAA16106.1; AUT_FRAME.		
DR	EMBL; AL021287; CAA16107.1; AUT_FRAME.		
DR	EMBL; AE007129; AAC17435.1; -.		
DR	TIGR; MT3106; -.		
DR	Tuberculist; Rv3022c; -.		
DR	InterPro; IPR000030; Microbac_PPE.		
DR	Hypothetical protein; Complete proteome.		
KW	G -> A (IN REF. 2).		
PT	CONFLICT 299 299 G -> VTCG (IN REF. 2).		
PT	CONFLICT 317 320 TAGV -> VTCG (IN REF. 2).		
PT	CONFLICT 326 326 V -> V (IN REF. 2).		
SQ	SEQUENCE 435 AA; 42876 MW; 3B157643EAA8184A CRC64;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CDC 1551 / Oshkosh;		
RX	Medline=96295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Bigmeier K., Gas S., Barry C.E. III, Tekata F., Badcock R., Utterback T., Weidman J.J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; Bacteriol. 184:5479-5490(2002).		
RA	Hypothesital PPE family protein Rv3429 OR MT3106 OR MT3533.		
RA	Mycobacterium tuberculosis		
RA	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.		
RA	[1] NCBI_TaxID=1773.		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=F137RV;		
RX	Medline=98226494; PubMed=12218036; Fleischmann R.D., Alland D., Eileen J.A., Carpenter L., White C., Kolonay J.F., Nelson W.C., Umayam L.A., Brzuska M., Salzberg S.L., Deicher A., Utterback T., Weidman J.J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; Bacteriol. 184:5479-5490(2002).		
RA	CC :-- SIMILARITY: Belongs to the mycobacterial PPE family.		
CC	-- CAUTION: Ref.1 sequence differs from that shown due to a framework in position 82.		
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DR	EMBL; AL021287; CAA16106.1; AUT_FRAME.		
DR	EMBL; AE007129; AAC17435.1; -.		
DR	TIGR; MT3106; -.		
DR	Tuberculist; Rv3022c; -.		
DR	InterPro; IPR000030; Microbac_PPE.		
DR	Hypothetical protein; Complete proteome.		
KW	G -> A (IN REF. 2).		
PT	CONFLICT 299 299 G -> VTCG (IN REF. 2).		
PT	CONFLICT 317 320 TAGV -> VTCG (IN REF. 2).		
PT	CONFLICT 326 326 V -> V (IN REF. 2).		
SQ	SEQUENCE 435 AA; 42876 MW; 3B157643EAA8184A CRC64;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CDC 1551 / Oshkosh;		
RX	Medline=98226494; PubMed=12218036; Fleischmann R.D., Alland D., Eileen J.A., Carpenter L., White C., Kolonay J.F., Nelson W.C., Umayam L.A., Brzuska M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,		

RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 laboratorial strains.";
 RL J. Bacteriol. 184:5479-5490(2002).

-!- SIMILARITY: Belongs to the mycobacterial PPE family.

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DR ENBML; A007158; AAK47873.1; -.
 DR PIR; C70975; C70975.
 DR MTGR; MN3533; -.
 DR Tuberculist; Rv34249; -.
 DR InterPro; IPR000030; Microbac_PPE.
 DR Pfam; PF00823; PPE; 1.
 DR Hypothetical protein; Complete proteome.

KW Hypothetical protein; Complete proteome.

SEQUENCE 178 AA; 1981 MW;

8BE1FC025ABFBAA6 CRC64;

DR Best Local Similarity 12.0%; Score 233.5; DB 1; Length 178;

DR Best Local Similarity 35.9%; Pred. No. 2.8e-07; Indels 76; Gaps 3;

DR Matches 65; Conservative 25; Mismatches 76; Indels 15; Gaps 3;

DR Qy 7 LPPIEINSANMYAGCGSASLIVAAQ---MWDS---VADSLSGASAFOQSVWGLTVGSSI 59

DR Db 5 IPAEYISNTIYEYGADSISSAAAELQRIMNNSANMTAKSLTDRLGEQE-----NWK 56

DR Qy 60 GSSAGLMLVAASAPVAVMSVTAGAELTAQVRVAAVAYETAVGLTPPVIAENRREL 119

DR Db 57 GSSSLMLAAGRYLDWLTKHSQILENLXVIVDLEIAYEEHKVYPPATIANNREBVH 116

DR Qy 120 ILIATNLGONTPAIVNAEYGMNWAQDAAMFGYAATAATATATLPEAPEPMTSAG 179

DR Db 117 RLIASNVAGNTPAITAGLIDAQYQQYRAQNIAVMDYQSTARFILAYLPWQEPFQIYGG 176

DR Qy 180 G 180

DR Db 177 G 177

RESULT 12 YY25 MYCTU STANDARD; PRT; 176 AA.

ID YY25 MYCTU STANDARD; PRT; 176 AA.

AC 050703; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-NOV-2001 (Rel. 40, Last annotation update)

DE Hypothetical PPE-family protein Rv3425.

GN RV3425 OR MTCY78_04C.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

CX NCBI_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96295987; PubMed=9634230;

RA Cole S.T., Broich R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Bigmeier K., Barry C.E., III, Tekia F.,

RA Badcock K., Besham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin T., Feitwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moulie S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

RA Rutten S., Seeger K., Shelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,

RT "Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";

RT Nature 393:537-544 (1998).

-!- SIMILARITY: Belongs to the mycobacterial PPE family.

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DR EMBL; Z77165; CAB0131.; -.

DR PIR; F70738; F70738.

DR Tuberculist; Rv3425; -.

DR InterPro; IPR00030; Microbac_PPE.

DR Pfam; PF00823; PPE; 1.

DR Hypothetical protein; Complete proteome.

DR Sequence 176 AA; 1985 MW;

B8CE229463BB7BD CRC64;

DR Best Local Similarity 11.2%; Score 217.5; DB 1; Length 176;

DR保守性 31; Mismatches 83; Indels 1; Gaps 1;

DR Matches 58; Conservative 31; Mismatches 83; Indels 1; Gaps 1;

DR Query 7 LPPIEINSANMYAGCGSASLIVAAQNDVSASLVSASLVSASLVSAGLM 66

DR 5 IPAEYISNTIYEYGADSLFLASGORELAYSVEETAESDELD-ENWKSSSDLL 63

DR 67 VAASSPYAMSVTAGQAELTAQAVRVAAYAETAYGLTPPPVTAENRABLMLIATNL 126

DR 64 ADAVEYXLOWSKHSSKOLKHEAWINGLNAYNDTRKVPPEEAANRERRIASNV 123

DR 127 LGONTPAIVNAEYGMWAAQDAAAMFGYAATAATATATLPEAPEPMTSAG 17.9

DR 124 AGVNTPAIADLDAQDQYQYARNVATMNAVSYWSWRSLSDLPWRPQPQTYRGG 17.6

DR RESULT 13 ELS_MOUSE STANDARD; PRT; 860 AA.

DR ID ELS_MOUSE STANDARD; PRT; 860 AA.

DR AC P54320; (Rel. 34, Created)

DR DT 01-OCT-1996 (Rel. 34, Last sequence update)

DR DT 10-OCT-2003 (Rel. 42, Last annotation update)

DR DE Elastin precursor (Troponelastin).

DR GN ELN.

DR OS Mus musculus (Mouse).

DR OC Muscarysota; Metaraco; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

DR OC NCBI_TaxID=10090;

DR OX [1] RN SEQUENCE FROM N.A.

DR STRAIN=BALB/c; TISSUE=Lung;

DR RX MEDLINE=95130069; PubMed=829060;

DR RA Wynder K.S., Sechler J.L., Boyd C.D., Passmore H.C.,

DR RT "use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human chromosome 7.";

DR Genomics 23:125-131 (1994).

DR CC 1- FUNCTION: Major structural protein of tissues such as aorta and

DR CC 2-mucosal ligament, which must expand rapidly and recover completely.

DR CC 1- SUBUNIT: The polymeric elastin chains are cross-linked together

DR CC 1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.

DR CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

DR CC the European Bioinformatics Institute. There are no restrictions on its

DR CC use by non-profit institutions as long as its content is in no way

DR CC modified and this statement is not removed. Usage by and for commercial

DR CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

DR CC or send an email to license@isb-sib.ch).

DR EMBL; U08210; AAR80155.1; -.

117	ELMIIATNLIGQNTPATIAVNEAYGENWAQDAAMFGYAAATAATATLIPPEAPEMT	176
487	-----GAGTGLMLVPG-----AVPGALPGAVGPALPGAVGPALP-GAVPGVP	527
177	SAGGLI-----BQAAVEEASDTAAANQMNVPQQLQLAQOPTGTTPSS-KLGJWKTYS	232
528	GTCGGPGACTPAALAAAAKAAA-----KAGQYGLGPVGCGVGVCGLPGGVG	579
233	PHRSPISNKMSMANNHMSVTINSGSM-TNTLSSMIKGF-APAAAQVQTAONGVRAMS	290
580	PG-----GVTGIGTGPGTGVPGDGGACTPAAKSAKAALAQAQYRAAA	624
291	SLGSIGSSGCGG-----AANIGRAASV--GSLSTYPOQAAANAOVTPARALPLT	341
625	GLGAGCPLGLGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	681
342	SLTSAEAERGPQOMLUGLPLPYCQMGARAG-GCLSGV	374
682	-----GGPGGLGPGGGLGPGGGFPGGPGLGGV	708

Search completed: August 25, 2004, 03:10:58
Job time : 28 secs

PIM: The crosslinks are made of deamidated lys.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2004, 03:13:09 ; Search time 127 Seconds

(without alignments)

967.510 Million cell updates/sec

Title: US-09-724-685-107

Perfect score: 1949

Sequence: 1 MVDFGALPPEINSARMYAGP.....SGYLRVDPFRPYVMPHSPAAAG 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters:

1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	1949	100.0	391	Sequence 14, App1
2	1949	100.0	391	Sequence 102, App
3	1949	100.0	391	Sequence 107, App
4	1949	100.0	391	Sequence 14, App1
5	1949	100.0	596	Sequence 26, App1
6	1949	100.0	596	Sequence 20, App1
7	1949	100.0	596	Sequence 26, App1
8	1949	100.0	596	Sequence 20, App1
9	1949	100.0	600	Sequence 22, App1
10	1949	100.0	600	Sequence 22, App1
11	1949	100.0	723	Sequence 2, App1
12	1949	100.0	729	Sequence 18, App1
13	1949	100.0	729	Sequence 18, App1
14	1949	100.0	729	Sequence 21, App1
15	1949	100.0	729	Sequence 22, App1

DESCRIPTION

SEQUENCE

Query Match 100.0%; Score 1949; DB 14; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.2e-145;
 Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60
 Db 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60

Qy 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60
 Db 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60

Qy 61 SSAGIMVAAAASPYYAVMSVTAQGAELTAQQRVAAAAYTAYGTYPVPIVIAENRAELMI 120
 Db 61 SSAGIMVAAAASPYYAVMSVTAQGAELTAQQRVAAAAYTAYGTYPVPIVIAENRAELMI 120

Qy 121 LIATNLIGONTPAIAVNEAEGYEMWAQDAAAMFGYAAATATAATATLPLPEEAPEMTSGG 180
 Db 121 LIATNLIGONTPAIAVNEAEGYEMWAQDAAAMFGYAAATATAATATLPLPEEAPEMTSGG 180

Qy 181 LLEQAAVEEASDTAAANQLMNPQALQLAQPTQGPSSKUJGGWTVSPRSPSN 240
 Db 181 LLEQAAVEEASDTAAANQLMNPQALQLAQPTQGPSSKUJGGWTVSPRSPSN 240

Qy 241 MVSMANNHMSMTNSGMNTLSMNLKGFAAAQAQVQTAONGVRAMSISLGSSG 300
 Db 241 MVSMANNHMSMTNSGMNTLSMNLKGFAAAQAQVQTAONGVRAMSISLGSSG 300

Qy 301 LGGGVAANLGRAASYGLSVPOAAVAAANOAVTPAARALPLTSLSAERGPQMLGGSLPV 360
 Db 301 LGGGVAANLGRAASYGLSVPOAAVAAANOAVTPAARALPLTSLSAERGPQMLGGSLPV 360

Qy 361 GQMGRAGGGLSGVLRVPBPYMPHSPAAAG 391
 Db 361 GQMGRAGGGLSGVLRVPBPYMPHSPAAAG 391

RESULT 3
 US-10-093-002-102
 Sequence 102, Application US/10193002
 Publication No. US2003013-026A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 Skeiky, Yasir A. W.
 Dillon, Davin C.
 Campos-Neto, Antonia
 Houghton, Raymond
 Veavick, Thomas S.
 Twardzik, Daniel R.
 Jode, Michael J.
 Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/193,002
 FILING DATE: 10-Jul-2002
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-May-1998

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-5031
 INFORMATION FOR SEQ ID NO: 102:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 102:

US-10-193-002-102

Query Match 100.0%; Score 1949; DB 14; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.2e-145;
 Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60
 Db 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60

Qy 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60
 Db 1 MVDFGALPPEINSARNYAGPGSASLIVAAQMWDSVADSFSAASAFQSTVWGLTVGSNG 60

Qy 61 SSAGIMVAAAASPYYAVMSVTAQGAELTAQQRVAAAAYTAYGTYPVPIVIAENRAELMI 120
 Db 61 SSAGIMVAAAASPYYAVMSVTAQGAELTAQQRVAAAAYTAYGTYPVPIVIAENRAELMI 120

Qy 121 LIATNLIGONTPAIAVNEAEGYEMWAQDAAAMFGYAAATATAATATLPLPEEAPEMTSGG 180
 Db 121 LIATNLIGONTPAIAVNEAEGYEMWAQDAAAMFGYAAATATAATATLPLPEEAPEMTSGG 180

Qy 181 LLEQAAVEEASDTAAANQLMNPQALQLAQPTQGPSSKUJGGWTVSPRSPSN 240
 Db 181 LLEQAAVEEASDTAAANQLMNPQALQLAQPTQGPSSKUJGGWTVSPRSPSN 240

Qy 241 MVSMANNHMSMTNSGMNTLSMNLKGFAAAQAQVQTAONGVRAMSISLGSSG 300
 Db 241 MVSMANNHMSMTNSGMNTLSMNLKGFAAAQAQVQTAONGVRAMSISLGSSG 300

Qy 301 LGGGVAANLGRAASYGLSVPOAAVAAANOAVTPAARALPLTSLSAERGPQMLGGSLPV 360
 Db 301 LGGGVAANLGRAASYGLSVPOAAVAAANOAVTPAARALPLTSLSAERGPQMLGGSLPV 360

Qy 361 GQMGRAGGGLSGVLRVPBPYMPHSPAAAG 391
 Db 361 GQMGRAGGGLSGVLRVPBPYMPHSPAAAG 391

RESULT 3
 US-10-094-843-107
 Sequence 107, Application US/10084843
 Publication No. US2003014-243A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 Skeiky, Yasir A. W.
 Dillon, Davin C.
 Campos-Neto, Antonio
 Houghton, Raymond
 Veavick, Thomas S.
 Twardzik, Daniel R.
 Lodes, Michael J.
 Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/094,843
 FILING DATE: 25-Feb-2002
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,967
 FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-5031
 INFORMATION FOR SEQ ID NO: 102:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 102:

US-10-193-002-102

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REFERENCE/DOCKET NUMBER: 210121-411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-084-843-107

Query Match 100.0% Score 1949; DB 14
Best Local Similarity 100.0% Pred. No. 1. 2e-14
Matches 391; Conservative 0; Mismatches 0;
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Ddb 1 MVDFGALPPEINSARMYAGPGSASLVAQAMQMDVSASDL
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61 SSAGGLMVAASPYAAMSVTAGQELTAQVRAAAAE
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181 LLEQAAAVEASDTAAANQLMNNYPOALQCOLAQPTGTT
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301 LGGGVAANIIGRAASVGSLISVPQAWAAACQAVTPAARALP
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361 GQM GARAGGGLGS37L RVP PRPYMPHSPAG 391

RESULT 4
US 10-098-732A-14
US 10-098-732A-14 Application US/10098732A
Publication No. US20130175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Co-  
leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US10/098,732A
CURRENT FILING DATE: 2003-04-19
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 14
LENGTH: 391
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: MTB39 full length (TbH9FL)
US-10-098-732A-14
Query Match 100.0% Score 1949; DB 14

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Best Local Similarity 100.0% ; Pred. No. 1.2e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 SSAGLMVAASPYAWMSVTAGQAELTAQVRVAAAAYETAGLTTPPPVIAENRAELMI 120
Db      61 SSAGLMVAASPYAWMSVTAGQAELTAQVRVAAAAYETAGLTTPPPVIAENRAELMI 120
Qy      121 LIATNLGLGONTPAJAVNEAEYGENWQDAAMFGYAAAATATAATLPLPFFEAPEMTSAGG 180
Db      121 LIATNLGLGONTPAJAVNEAEYGENWQDAAMFGYAAAATATAATLPLPFFEAPEMTSAGG 180
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Db      181 LLEQAAAVEASDAAANQLMNNVPOALQOLOAQPQTGTTPSSKLGGLWKTVSPHSPISN 240
Qy      241 MVSVANNIMNSMTNSGVSMNTLSSMLKGFPAPAAAQQAVOTAQNGVRAMSSLGSSIGSSG 300
Db      241 MVSVANNIMNSMTNSGVSMNTLSSMLKGFPAPAAAQQAVOTAQNGVRAMSSLGSSIGSSG 300
Qy      301 LGGGVAAANLGRAASVGSLSVPOAAQANQAVTPAARALPLTSLSLTSAAERGPQMLGLPV 360
Db      301 LGGGVAAANLGRAASVGSLSVPOAAQANQAVTPAARALPLTSLSLTSAAERGPQMLGLPV 360
Qy      361 GQMGRAGGLSGVLRVPVRPPYVMHPSPAG 391
Db      361 GQMGRAGGLSGVLRVPVRPPYMEHSPAG 391

RESULT 5
US-09-287-849-26
; Sequence 26, Application US/09287849
; Patent No. US20020009459A1
; GENERAL INFORMATION.
; APPLICANT: Reed, Steven G.
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Nato, Antonio
; APPLICANT: Corixia Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 09/056,556
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 26
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26

Query Match 100.0% ; Score 1949; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-09-287-849-26

Query Match 100.0% ; Score 1949; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-145;
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US-09-287-849-26

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Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-09-287-849-26

Query Match 100.0% ; Score 1949; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-09-287-849-26

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RESULT 6
 US-09-886-349A-20
 ; Sequence 20, Application US/09886349A
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir
 ; REED, Steven
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 ; FILE REFERENCE: 014-058-00902020US
 ; CURRENT APPLICATION NUMBER: US/10/359,460
 ; PRIORITY FILING DATE: 2003-02-05
 ; PRIORITY APPLICATION NUMBER: US/09/287,849
 ; PRIORITY FILING DATE: 1999-04-07
 ; PRIORITY APPLICATION NUMBER: US/09/287,849
 ; PRIORITY FILING DATE: 1997-03-13
 ; PRIORITY APPLICATION NUMBER: US/08/942,578
 ; PRIORITY FILING DATE: 1997-10-01
 ; PRIORITY APPLICATION NUMBER: US/09/025,197
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US/09/056,556
 ; PRIORITY FILING DATE: 1998-04-07
 ; PRIORITY APPLICATION NUMBER: US/09/223,040
 ; PRIORITY FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 26
 ; LENGTH: 596
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
 ; OTHER INFORMATION: protein TbH9-Ra35 (designated Mtb59?)
 ; SEQ ID NO: 20
 ; LENGTH: 596
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
 ; OTHER INFORMATION: protein TbH9-Ra35 (designated Mtb59?)
 ; SEQ ID NO: 20
 ; LENGTH: 596
 ; Score: 1949; DB: 12; Length: 596;
 ; Best Local Similarity: 100.0%; Pred. No.: 2e-145;
 ; Matches: 391; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 ; Query Match: 1 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Db: 9 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Qy: 1 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Db: 9 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Qy: 61 SSAGLMVAAASPYAAMSVTAGAELTAQRVAAAYETYGLTVPPVIAENRAELMI 120
 ; Db: 69 SSAGLMVAAASPYAAMSVTAGAELTAQRVAAAYETYGLTVPPVIAENRAELMI 120
 ; Qy: 121 LIATNLIGONTPATIAVNEAEYGMWADAAAMFGYAAATAATATLPPFEAVENTSAGG 180
 ; Db: 129 LIATNLIGONTPATIAVNEAEYGMWADAAAMFGYAAATAATATLPPFEAVENTSAGG 188
 ; Qy: 181 LLEQQAAVEEASDTRAANQMLNNVPQALQLAQPTQGTTPSSKLGGLWKTSPHSRSPISN 240
 ; Db: 189 LLEQQAAVEEASDTRAANQMLNNVPQALQLAQPTQGTTPSSKLGGLWKTSPHSRSPISN 248
 ; RESULT 7
 ; US-10-359-460-26
 ; Sequence 26, Application US/10359460
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A. N.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Campos Neto, Antonio
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 ; FILE REFERENCE: 014-058-00902020US
 ; CURRENT APPLICATION NUMBER: US/10/359,460
 ; PRIORITY FILING DATE: 2003-02-05
 ; PRIORITY APPLICATION NUMBER: US/09/287,849
 ; PRIORITY FILING DATE: 1999-04-07
 ; PRIORITY APPLICATION NUMBER: US/09/287,849
 ; PRIORITY FILING DATE: 1997-03-13
 ; PRIORITY APPLICATION NUMBER: US/08/942,578
 ; PRIORITY FILING DATE: 1997-10-01
 ; PRIORITY APPLICATION NUMBER: US/09/025,197
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US/09/056,556
 ; PRIORITY FILING DATE: 1998-04-07
 ; PRIORITY APPLICATION NUMBER: US/09/223,040
 ; PRIORITY FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 26
 ; LENGTH: 596
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
 ; US-10-359-460-26
 ; Query Match: 1 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Db: 9 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Qy: 1 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Db: 9 MVDGFALPPEINSARMYAGPGSASLVAQWMDSVASDLFSAASAQSYYVGLTVGIG
 ; Qy: 61 SSAGLMVAAASPYAAMSVTAGAELTAQRVAAAYETYGLTVPPVIAENRAELMI 120
 ; Db: 69 SSAGLMVAAASPYAAMSVTAGAELTAQRVAAAYETYGLTVPPVIAENRAELMI 128
 ; Qy: 121 LIATNLIGONTPATIAVNEAEYGMWADAAAMFGYAAATAATATLPPFEAVENTSAGG 180
 ; Db: 129 LIATNLIGONTPATIAVNEAEYGMWADAAAMFGYAAATAATATLPPFEAVENTSAGG 188
 ; Qy: 181 LLEQQAAVEEASDTRAANQMLNNVPQALQLAQPTQGTTPSSKLGGLWKTSPHSRSPISN 240
 ; Db: 189 LLEQQAAVEEASDTRAANQMLNNVPQALQLAQPTQGTTPSSKLGGLWKTSPHSRSPISN 248

Publication No. US20030147911A1
 GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis Antigens
 ; FILE REFERENCE: 014058-0059081US
 CURRENT APPLICATION NUMBER: US/10/359,460
 PRIOR APPLICATION NUMBER: US/09/287,849
 ; PRIOR FILING DATE: 1999-04-07
 ; PRIOR APPLICATION NUMBER: US 08/818,112
 ; PRIOR FILING DATE: 1997-03-13
 ; PRIOR APPLICATION NUMBER: US 08/947,578
 ; PRIOR FILING DATE: 1997-10-01
 ; PRIOR APPLICATION NUMBER: US 09/025,197
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 09/056,556
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 09/223,040
 ; PRIOR FILING DATE: 1998-12-30
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 22
 LENGTH: 600
 TYPE: PTI
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
 US-10-359-460-22

Query Match 100.0% Score 1949; DB 15; Length 600;
 Best Local Similarity 100.0%; Pred. No. 2, 5e-145;
 Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVDFGALPPEINSARMYAGPGSASLVAQQMWDPSVASDILFSAASAFOQVVWGLTVGSWIG 60
 Db 333 MVDFGALPPEINSARMYAGPGSASLVAQQMWDPSVASSDILFSAASAFOQVVWGLTVGSWIG 392

Qy 61 SSAGIMVAASPYAAMVSSTAGAELTAQVRAAYBTAXGLTVPPVIAENRAELMI 120
 Db 393 SSAGIMVAASPYAAMVSSTAGAELTAQVRAAYBTAXGLTVPPVIAENRAELMI 452

Qy 121 LIATNLIGONTPALAVNAEYGEMWAQDAAMGYAAATAATATLIFEEAPEMTSGG 180
 Db 453 LIATNLIGONTPALAVNAEYGEMWAQDAAMGYAAATAATATLIFEEAPEMTSGG 512

Qy 181 LLEQAAAYEEASDTAAANQLMNVPQAIQLQOPTGTPSKLGGIWKTVSPHRSPI 240
 Db 513 LLEQAAAYEEASDTAAANQLMNVPQAIQLQOPTGTPSKLGGIWKTVSPHRSPI 572

Qy 241 MVSHANNHMSMTNSGVSTINTLSMLKGFAAAAEYGMWAQDAAMGYAAQVTAQONGVRAMSSGSSG 300
 Db 573 MVSHANNHMSMTNSGVSTINTLSMLKGFAAAAEYGMWAQDAAMGYAAQVTAQONGVRAMSSGSSG 632

Qy 301 LGGGVAANLGRASVGSGSISVPOWAANQAVTPAARALPLTSLSAERGPQMLGGLPV 360
 Db 633 LGGGVAANLGRASVGSGSISVPOWAANQAVTPAARALPLTSLSAERGPQMLGGLPV 692

Qy 361 GONGGARAGGGLSGVLRVPPRYVMPHSPAG 391
 Db 693 GONGGARAGGGLSGVLRVPPRYVMPHSPAG 723

RESULT 12
 US-09-886-349A-18
 ; Sequence 18, Application US/09886349A
 ; Publication No. US20040086523A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Reed, Steven
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 ; FILE REFERENCE: 014058-0059081US
 CURRENT APPLICATION NUMBER: US/09/886,349A
 ; PRIOR APPLICATION NUMBER: US 09/597,796
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: US 60/265,737
 ; PRIOR FILING DATE: 2001-02-01
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.1

RESULT 11
 US-10-369-983-2
 ; Sequence 2, Application US/10369983
 ; Publication No. US20031235593A1
 ; GENERAL INFORMATION:

SEQ ID NO 18
 LENGTH: 729
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA
 OTHER INFORMATION: (Rai2-TBhp-Ra35MutSA)
 US-09-886-349A-18

Query Match: 100.0%; Score 1949; DB 12; Length 729;
 Best Local Similarity: 100.0%; Pred. No. 2 6e-145; Indels 0; Gaps 0;
 Matches 391; Conservative 0; Mismatches 0;

Qy 1 MVDFGALPPEINSARMYAGPGSASLVLAAQMQMDSVADLSAASAFAQSYYWGLTVGSWIG 60
 Db 142 MVDFGALPPEINSARMYAGPGSASLVLAAQMQMDSVADLSAASAFAQSYYWGLTVGSWIG 201

Qy 61 SSAGIMVAASPYAMSVTAGQELTAQVRAAAAYETAYGLTVPPVIAENRAELMI 120
 Db 202 SSAGIMVAASPYAMSVTAGQELTAQVRAAAAYETAYGLTVPPVIAENRAELMI 261

Qy 121 LIATNLGQNTPAIAYNEAEYGEMWAQDAAAAMFGYAATAATATLPLFEAPEMTSAGG 180
 Db 262 LIATNLGQNTPAIAYNEAEYGEMWAQDAAMFGYAATAATATLPLFEAPEMTSAGG 321

Qy 181 LIEQAAAVEASDAAANOLMNVPOALQOLAOPTCGTTPSSKLGWKLTKVSPHRSPISN 240
 Db 322 LIEQAAAVEASDAAANOLMNVPOALQOLAOPTCGTTPSSKLGWKLTKVSPHRSPISN 381

Qy 241 MVSMANNHMSMTNSGVSMTNTLSMLKGAPAAAQAQVTAQNGVRAMSISSSG 300
 Db 382 MVSMANNHMSMTNSGVSMTNTLSMLKGAPAAAQAQVTAQNGVRAMSISSSG 441

Qy 301 LGGGVAANLGRAASVGSLSYPOQAAANGAVTPAARALPLTSLSAERGPQMLGGLPV 360
 Db 442 LGGGVAANLGRAASVGSLSYPOQAAANGAVTPAARALPLTSLSAERGPQMLGGLPV 501

Qy 361 GQMGRAGGGISGVLRVPRPPYMPHSPIAG 391
 Db 502 GQMGRAGGGISGVLRVPRPPYMPHSPIAG 532

RESULT 14
 US-10-369-983-21
 ; Sequence 21, Application US/10369983
 ; Publication No. US20010235593A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Guderian, Jeff
 ; APPLICANT: Reed, Steven
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 ; CURRENT APPLICATION NUMBER: US10/369,983
 ; FILE REFERENCE: 014058-00081US
 ; CURRENT FILING DATE: 2003-02-18
 ; PRIORITY NUMBER: US 60/357,351
 ; PRIORITY FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 21
 ; LENGTH: 729
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:MTB72F
 US-10-369-983-21

Query Match: 100.0%; Score 1949; DB 15; Length 729;
 Best Local Similarity: 100.0%; Pred. No. 2.6e-145; Indels 0; Gaps 0;

Qy 1 MVDFGALPPEINSARMYAGPGSASLVLAAQMQMDSVADLSAASAFAQSYYWGLTVGSWIG 60
 Db 142 MVDFGALPPEINSARMYAGPGSASLVLAAQMQMDSVADLSAASAFAQSYYWGLTVGSWIG 201

Qy 61 SSAGIMVAASPYAMSVTAGQELTAQVRAAAAYETAYGLTVPPVIAENRAELMI 120
 Db 202 SSAGIMVAASPYAMSVTAGQELTAQVRAAAAYETAYGLTVPPVIAENRAELMI 261

Qy 121 LIATNLGQNTPAIAYNEAEYGEMWAQDAAAAMFGYAATAATATLPLFEAPEMTSAGG 180
 Db 262 LIATNLGQNTPAIAYNEAEYGEMWAQDAAMFGYAATAATATLPLFEAPEMTSAGG 321

Qy 181 LIEQAAAVEASDAAANOLMNVPOALQOLAOPTCGTTPSSKLGWKLTKVSPHRSPISN 240
 Db 322 LIEQAAAVEASDAAANOLMNVPOALQOLAOPTCGTTPSSKLGWKLTKVSPHRSPISN 381

RESULT 15
 US-10-098-732A-18
 ; Sequence 18, Application US/10098732A
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Brannon, Mark
 ; APPLICANT: Guderian, Jeffrey
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
 ; FILE REFERENCE: 014058-012201019
 ; CURRENT APPLICATION NUMBER: US20030175294A1
 ; PRIOR APPLICATION NUMBER: US 60/275,837
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 18
 ; LENGTH: 729
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA
 ; OTHER INFORMATION: (Rai2-TBhp-Ra35MutSA)
 US-10-098-732A-18

Query Match: 100.0%; Score 1949; DB 14; Length 729;
 Best Local Similarity: 100.0%; Pred. No. 2.6e-145; Indels 0; Gaps 0;

Search Completed: August 25, 2004, 03:28:09
 Job Time : 131 secs

RESULT 15
 US-10-369-983-22

Sequence 22, Application US/10369983
 Publication No. US20030235593A1

GENERAL INFORMATION:

APPLICANT: Skeiry, Yasir
 APPLICANT: Guderian, Jeff
 APPLICANT: Reed, Steven

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 01408-009081US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 22

LENGTH: 729

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: mutated
 OTHER INFORMATION: MTb72FmutsA (Mtbo72F-mutsA)

US-10-369-983-22

Query Match 100.0%; Score 194; DB 15; Length 729;
 Best Local Similarity 100.0%; Pred. No. 2. 6e-145;
 Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVDFGALPPBEINSARMYAGPGASLVAQQWDSVASDLSFSAASAFOSVWGLTYGSWIG 60
 Db 142 MVDFGALPPBEINSARMYAGPGASLVAQQWDSVASDLSFSAASAFOSVWGLTYGSWIG 201

Qy 61 SSAGLMVIAASAPVYAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
 Db 202 SSAGLMVIAASAPVAMMVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261

Qy 121 LIATNLIGONTPAJAVNEAEYGEMWAQDAAAAMEGYAAATAATATLPPFEDAPEMTSAGG 180
 Db 262 LIATNLIGONTPAJAVNEAEYGEMWAQDAAAAMEGYAAATAATATLPPFEDAPEMTSAGG 321

Qy 181 LLIQQAEEVEASDTAAANQLNNVPQLQQLAQPTGTTPSSRLGGIWKTVSPHSPISPIN 240
 Db 322 LLRQQAEEVEASDTAAANQLNNVPQLQQLAQPTGTTPSSKLGGIWKTVSPHSPISPIN 381

Qy 241 MVSMANNIMSMINTSGVSMNTLSSMLKGFAAAAAQAVOTAAQNGYRAMSSLGSSLGSSG 300
 Db 382 MVSMANNIMSMINTSGVSMNTLSSMLKGFAAAAAQAVOTAAQNGYRAMSSLGSSLGSSG 441

Qy 301 LGGGVAANLGRASVGSLSPVQWAAANQVTPAARALPLTSLSAERGFCQMGGLPV 360
 Db 442 LGGGVAANLGRASVGSLSPVQWAAANQVTPAARALPLTSLSAERGFCQMGGLPV 501

Qy 361 GONGARAGGGLSCGVLRVPPRYMPISPAAG 391
 Db 502 GONGARAGGGLSCGVLRVPPRYMPISPAAG 532

GenCore version 5.1.6					
Copyright (c) 1993 - 2004 Compugen Ltd.					
Protein search, using SW model					
on: August 25, 2004, 02:57:18 ; Search time 128 Seconds (without alignments)					
863.094 Million cell updates/sec					
file: US-09-724-685-107					
exact score: 1949					
length: 1 MVDDGALPBEINSSARMYAGP SGVLRVPPRPPYVMPHSPAAAG 391.					
scoring table: BLOSUM62					
gap cost: Gapop 10.0 , Gapext 0.5					
checked: 1586107 seqs, 282547505 residues					

ALIGNMENTS

RESULT 1

T 1
381
RAW32381 standard; protein; 391 AA.
RAW32381;
113-JAN-1998 (first entry)
Mycobacterium tuberculosis antigen TbH-9FL.
Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
skin testing; M.tuberculosis.
Mycobacterium tuberculosis.

SUMMARY

result	Query				DB	ID	Description
	No.	Score	Match	Length			
1	1949	100.0	391	2	AAW33381		Mycobacte
	2	1949	100.0	391	2	AAW32449	Mycobacte
	3	1949	100.0	391	2	AAW64335	Mycobacte
	4	1949	100.0	391	2	AAWB1702	M. tuberc
	5	1949	100.0	391	2	AAY04778	Mycobacte
	6	1949	100.0	391	2	AAY38898	M. tuberc
	7	1949	100.0	391	2	AAY39132	M. tuberc
	8	1949	100.0	391	4	AAU01888	M. tuberc
	9	1949	100.0	391	5	AAE29107	Mycobacte
	10	1949	100.0	391	5	AEE17511	Mycobacte
	11	1949	100.0	596	2	AAY32010	Mycobacte
	12	1949	100.0	596	5	AAE29710	Mycobacte
	13	1949	100.0	596	5	AEE17574	Mycobacte
	14	1949	100.0	599	5	AAU74599	Antigenic
	15	1949	100.0	600	2	AAY32268	Mycobacte
	16	1949	100.0	600	5	AAU74597	Antigenic
	17	1949	100.0	723	7	ADA26354	Mycobacte
	18	1949	100.0	729	4	AAO22142	Ral2-H9-3
	19	1949	100.0	729	5	AAE29709	Mycobacte
	20	1949	100.0	729	5	AEE17573	Mycobacte
	21	1949	100.0	729	7	ADA26374	Mycobacte
	22	1949	100.0	744	5	AAU01912	M. tuberc
	23	1949	100.0	813	7	ADA26367	Mycobacte
	24	1949	100.0	815	4	AAU01904	M. tuberc
	25	1949	100.0	826	5	ADA26352	Mycobacte
	26	1949	100.0	826	5	ADA26353	Mycobacte

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMATES

A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M. tuberculosis antigen, TbHgP1. The immunogenic polypeptide can be used to diagnose M. tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the agents that bind to the antigen, used as diagnostic primers or probes and the agents that bind to the antigen,

DE	XX	M. tuberculosis immunogenic polypeptide TbH-9FL.
PR	XX	XX Tuberculosis; immunogenic; soluble antigen; protective immunity; TB;
XX	KW	vaccine; pharmaceutical; infection; diagnosis.
PA	XX	
PI	PI	(CORIXA) CORIXA CORP.
XX	XX	
XX	XX	Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX	XX	Vedvick TS, Twardzik DR, Lodes MJ;
XX	XX	WPI: 1998-251292/22.
XX	XX	N-PSDB; AAV44395.
PT	PT	New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
PT	PT	Example 3; Page 133-135; 250pp; English.
XX	XX	This polypeptide comprises Mycobacterium tuberculosis antigen TbH-9FL. It is encoded by genomic DNA (see AAV44395) isolated from a M. tuberculosis strain H37Rv genomic library using a probe from clone TbH-9 (see AAV44371). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAV44291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides. Recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
XX	XX	CC This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (Mtb) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
CC	CC	Example 3B; Page 128-129; 230pp; English.
PS	PS	Example 3C; Page 128-129; 230pp; English.
XX	XX	This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (Mtb) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
CC	CC	Sequence 391 AA;
CC	CC	Query Match Score 1949; DB 2; Length 391;
CC	CC	Best Local Similarity 100.0%; Pred. No. 1.2e-142; Mismatches 0; Indels 0; Gaps 0;
CC	CC	Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	CC	Sequence 391 AA;
XX	XX	Query Match Score 1949; DB 2; Length 391;
Db	Db	Best Local Similarity 100.0%; Pred. No. 1.2e-142; Mismatches 0; Indels 0; Gaps 0;
Qy	Qy	Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	Db	1 MYDFGALPEINSARMYAGPGSÁLVAQMDVSADLFSAASAFQSYVWGLTVGSWIG 60
Qy	Qy	61 SSAGLMYAAASPYVAMSVTACQELTAQVRVALAYETAYGLTVPPVIAENRAELMI 120
Db	Db	61 SSAGLMYAAASPYVAMSVTACQELTAQVRVALAYETAYGLTVPPVIAENRAELMI 120
Qy	Qy	121 LIATNLIGONTPAIVNEAYGEMWAQDAAMFGYAAATATATLPLPEEAPENTSAGG 180
Db	Db	121 LIATNLIGONTPAIVNEAYGEMWAQDAAMFGYAAATATATLPLPEEAPENTSAGG 180
Qy	Qy	181 LIEQQAAYVEASDAAANQMLNNVPQAIQLAQOPTCTPSSKLGGIWKTVSPHSPISN 240
Db	Db	181 LIEQQAAYVEASDAAANQMLNNVPQAIQLAQOPTCTPSSKLGGIWKTVSPHSPISN 240
Qy	Qy	241 MYSMANNHMSMTNSGVSMNTLSSMLKGFAAAAAQVTAQNGYRAMSSLGSG 300
Db	Db	241 MYSMANNHMSMTNSGVSMNTLSSMLKGFAAAAAQVTAQNGYRAMSSLGSG 300
Qy	Qy	301 LGGGVAANLGRASAVGSISVPOWAANAOVTPAARALPLTSUTSAERGPQMLGGIPV 360
Db	Db	301 LGGGVAANLGRASAVGSISVPOWAANAOVTPAARALPLTSUTSAERGPQMLGGIPV 360
Qy	Qy	361 GONGCARGAGGLSEVTRVPPRPMPHSAAAG 391
Db	Db	361 GONGCARGAGGLSEVTRVPPRPMPHSAAAG 391
RESULT 4		AAM81702
ID		AAM81702 standard; protein; 391 AA.
XX		AC AAM81702
XX		361 GOMGARAGGGISGVLRVPPRPMHSPAG 391
XX		361 GOMGARAGGGISGVLRVPPRPMHSPAG 391

AY04778	AAV04778 standard; protein; 391 AA.	QY	361 GQM GARAGGGILSGVLRVPPR PYNMPHSPAG 391
XX		Db	361 GQM GARAGGGILSGVLRVPPR PYNMPHSPAG 391
AC			
XX			
DT	06-JUL-1999 (first entry)		
XX	Mycobacterium species protein sequence 5R.	RESULT 6	
XX	Secreted protein; Mycobacterium; primer; PCR; amplification; probe;	AAY38989	
KW	hybridisation; detection; vaccine; immunisation; infection.	ID AAY38989 standard; protein; 391 AA.	
XX	Mycobacterium sp.	XX	
OS		AC AAY38989;	
PN		XX	
XX		DT 05-NOV-1999 (first entry)	
PD	25-FEB-1999.	XX	
XX	Antigen; diagnosis; detection; infection; antibody; immunisation;	DE M. tuberculosis recombinant antigen protein TbH-9FL.	
PF	14-AUG-1998; 98WO-FR001813.	XX	
XX	XX	XX	
PR	14-AUG-1997; 97FR-00010404.	OS Mycobacterium tuberculosis.	
PR	11-SEP-1997; 97FR-00011325.	XX	
XX		PN WO942118-A2.	
PA	(INSP) INST PASTEUR.	XX	
PT	Gicquel B, Portnoie D, Lim E, Pellicic V, Guiugueno A;	PD 26-AUG-1999.	
PI	Goguet De La Salmoniere Y;	XX	
XX		XX	
DR	WPI: 1999-181045/15.	PF 17-FEB-1999;	99WO-US003265.
DR	N-PSDB, AAX34030.	XX	
XX		XX	
PT	Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.	PR 18-FEB-1998;	98US-00024753.
PT	XX	PR 05-MAY-1998;	98US-00072596.
TR		XX	
XX		PA (CORI-) CORIXA CORP.	
XX		XX	
CC	Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.	PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;	
CC	Sequence 391 AA;	PI Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;	
CC		XX	
CC		DR WPI: 1999-527416/44.	
CC		DR N-PSDB; AAZ19093.	
CC		XX	
CC	Query Match Score 100.0%; DB 2; Length 391;	PT New polypeptide comprising antigenic portions of M. tuberculosis.	
CC	Best Local Similarity 100.0%; Pred. No. 1.2e-142;	XX	
CC	Matches 391; Conservative 0; Mismatches 0; Gaps 0;	PS Example 3; Page 168-169; 323pp; English.	
CC		XX	
CC	This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.	XX	
CC	Sequence 391 AA;	SQ Sequence 391 AA;	
CC		Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 1.2e-142; Matches 391; Conservative 0; Mismatches 0; Gaps 0;	
CC		SQ Sequence 391 AA;	
CC	1 MVDFGALPPEINSARMYAGPGSASLYVAAQMDVSADLFSASAFAQSIVWGLTVGSWTG 60	1 MVDFGALPPEINSARMYAGPGSASLYVAAQMDVSADLFSASAFAQSIVWGLTVGSWTG 60	1 MVDFGALPPEINSARMYAGPGSASLYVAAQMDVSADLFSASAFAQSIVWGLTVGSWTG 60
CC	61 SSAGIMVAASAPYVAVMSVTGAQAOELTAQAVRVAAAAYETAYGTIVPPVIAENRAELM 120	61 SSAGIMVAASAPYVAVMSVTGAQELTAQAVRVAAAAYETAYGTIVPPVIAENRAELM 120	61 SSAGIMVAASAPYVAVMSVTGAQELTAQAVRVAAAAYETAYGTIVPPVIAENRAELM 120
CC	61 SSAGIMVAASAPYVAVMSVTGAQELTAQAVRVAAAAYETAYGTIVPPVIAENRAELM 120	1 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180	1 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180
CC	121 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180	121 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180	121 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180
CC	121 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180	121 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180	121 LIATNLQLQNTPAIAVNEAEGYEMQAQDAAAMEGYAAATAATATLPPBEEAPEMTSAGC 180
CC	181 LLEQAAAVEEASDAAANQLMNNYPOALQOLAQOPTGTTPSKKGILWKTVPSPRSPI 240	181 LLEQAAAVEEASDAAANQLMNNYPOALQOLAQOPTGTTPSKKGILWKTVPSPRSPI 240	181 LLEQAAAVEEASDAAANQLMNNYPOALQOLAQOPTGTTPSKKGILWKTVPSPRSPI 240
CC	181 LLEQAAAVEEASDAAANQLMNNYPOALQOLAQOPTGTTPSKKGILWKTVPSPRSPI 240	181 LLEQAAAVEEASDAAANQLMNNYPOALQOLAQOPTGTTPSKKGILWKTVPSPRSPI 240	181 LLEQAAAVEEASDAAANQLMNNYPOALQOLAQOPTGTTPSKKGILWKTVPSPRSPI 240
CC	241 MVSMANNHMSMTNSGYSMMTLLSSMLKGAPAAAQAYQTAAQNGVRAMSLGSSLGSSG 300	241 MVSMANNHMSMTNSGYSMMTLLSSMLKGAPAAAQAYQTAAQNGVRAMSLGSSLGSSG 300	241 MVSMANNHMSMTNSGYSMMTLLSSMLKGAPAAAQAYQTAAQNGVRAMSLGSSLGSSG 300
CC	241 MVSMANNHMSMTNSGYSMMTLLSSMLKGAPAAAQAYQTAAQNGVRAMSLGSSLGSSG 300	241 MVSMANNHMSMTNSGYSMMTLLSSMLKGAPAAAQAYQTAAQNGVRAMSLGSSLGSSG 300	241 MVSMANNHMSMTNSGYSMMTLLSSMLKGAPAAAQAYQTAAQNGVRAMSLGSSLGSSG 300
CC	301 LGGGVAAANLGRAASYGVLSSLYQPAWAANGQAVTAQNGVRAMSLGSSLGSSG 360	301 LGGGVAAANLGRAASYGVLSSLYQPAWAANGQAVTAQNGVRAMSLGSSLGSSG 360	301 LGGGVAAANLGRAASYGVLSSLYQPAWAANGQAVTAQNGVRAMSLGSSLGSSG 360
CC	301 LGGGVAAANLGRAASYGVLSSLYQPAWAANGQAVTAQNGVRAMSLGSSLGSSG 360	301 LGGGVAAANLGRAASYGVLSSLYQPAWAANGQAVTAQNGVRAMSLGSSLGSSG 360	301 LGGGVAAANLGRAASYGVLSSLYQPAWAANGQAVTAQNGVRAMSLGSSLGSSG 360

Best Local Similarity 100.0%; Pred. No. 1.2e-142; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVDFGALPPEINSARMYAGPGSASLVAACQMDSVASDLFSAASAFAQSVMGLTVGSWIG 60
 Db 1 MVDFGALPPEINSARMYAGPGSASLVAACQMDSVASDLFSAASAFAQSVMGLTVGSWIG 60
 Qy 61 SSAGLMVAAASPYYAAMSYSTAGQELTAACQVRVAAAYETAYGTIVPPVIAENRAELMI 120
 Db 61 SSAGLMVAAASPYYAAMSYSTAGQELTAACQVRVAAAYETAYGTIVPPVIAENRAELMI 120
 Qy 121 LIATNLGONTPAIANNEAYGEMQAQDAMGYAAATAATATLPEADEMTSAGG 180
 Db 121 LIATNLGONTPAIANNEAYGEMQAQDAMGYAAATAATATLPEADEMTSAGG 180
 Qy 181 LLEQQAEEBAASDTAAANQMLNNPQALQOQAQPTQGTPSSKGJLWKTSPHRSPLSN 240
 Db 181 LLEQQAEEBAASDTAAANQMLNNPQALQOQAQPTQGTPSSKGJLWKTSPHRSPLSN 240
 Qy 241 MVSMANNNSMTNSCVSMNTLSSMLKGFPAAPAAAQVOTAAONGVRAMSSLGSSLGSSG 300
 Db 241 MVSMANNNSMTNSCVSMNTLSSMLKGFPAAPAAAQVOTAAONGVRAMSSLGSSLGSSG 300
 Qy 301 LGGGYAANLGRAASVGSLSVPOAAWAANQAVTAAARALPLTSLSAERGPQMLGGLPV 360
 Db 301 LGGGYAANLGRAASVGSLSVPOAAWAANQAVTAAARALPLTSLSAERGPQMLGGLPV 360
 Qy 361 GOMGARAGGGSGVLRPPRYPMPHSAAAG 391
 Db 361 GOMGARAGGGSGVLRPPRYPMPHSAAAG 391

RESULT 9
 AAE29707 ID AAE29707 standard; protein; 391 AA.
 XX AC AAE29707;
 DT 27-JAN-2003 (first entry)
 DE Mycobacterium sp. TbH9FL antigenic protein.
 XX Vaccine; immunity; diagnostic agent; gene therapy; TbH9FL antigen.
 XX Mycobacterium sp.
 CS PN WO200272792-A2.
 XX PD 19-SEP-2002.
 XX PF 13-MAR-2002; 2002WO-US008223.
 XX PR 13-MAR-2001; 2001US-0275837P.
 XX PA (CORI-X) CORIXA CORP.
 XX DR 2002-759844/82.
 XX DR N-PSDB; AAD47082.

PS Disclosure: Page 86-87; 155pp; English.
 XX PT New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,
 CC fusion polypeptide. The recombinant nucleic acid comprises a heterologous
 CC M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
 PT against pathogenic microorganisms e.g. Leishmania and Mycobacterium
 PT tuberculosis.
 XX PS The invention relates to a recombinant nucleic acid molecule encoding a
 CC fusion polypeptide. The recombinant nucleic acid comprises a heterologous
 CC polynucleotide sequence encoding an antigen or an antigenic fragment from
 CC Mycobacterium sp. and Leishmania Polynucleotide sequence encoding a
 CC polypeptide or its fragment. The Leishmania Polynucleotide is selected

CC from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention
 CC are used in methods for eliciting immune response in mammals. They are
 CC useful as vaccines to elicit protective immunity against pathogenic
 CC microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
 CC polypeptides are used for enhancing the expression of Polynucleotides, as
 CC in vivo diagnostic agents and for raising antibodies in a non-human
 CC animal. The invention is used in gene therapy. The present sequence is
 CC Mycobacterium sp. TbH9FL antigenic protein
 XX Sequence 391 AA;

Query Match	100.0%	Score 1919;	DB 5;	Length 391;
Best Local Similarity	100.0%	Pred. No. 1.2e-142;	Mismatches 0;	Indels 0;
Matches 391;	Conservative 0;	N mismatches 0;	Gaps 0;	
Qy	1 MVDFGALPPEINSARMYAGPGSASLVAACQMDSVASDLFSAASAFAQSVMGLTVGSWIG 60	Db	1 MVDFGALPPEINSARMYAGPGSASLVAACQMDSVASDLFSAASAFAQSVMGLTVGSWIG 60	
Qy	1 MVDFGALPPEINSARMYAGPGSASLVAACQMDSVASDLFSAASAFAQSVMGLTVGSWIG 60	Db	1 MVDFGALPPEINSARMYAGPGSASLVAACQMDSVASDLFSAASAFAQSVMGLTVGSWIG 60	
Qy	61 SSAGLMVAAASPYYAAMSYSTAGQELTAACQVRVAAAYETAYGTIVPPVIAENRAELMI 120	Db	61 SSAGLMVAAASPYYAAMSYSTAGQELTAACQVRVAAAYETAYGTIVPPVIAENRAELMI 120	
Qy	61 SSAGLMVAAASPYYAAMSYSTAGQELTAACQVRVAAAYETAYGTIVPPVIAENRAELMI 120	Db	61 SSAGLMVAAASPYYAAMSYSTAGQELTAACQVRVAAAYETAYGTIVPPVIAENRAELMI 120	
Qy	121 LIATNLGONTPAIANNEAYGEMQAQDAMGYAAATAATATLPEADEMTSAGG 180	Db	121 LIATNLGONTPAIANNEAYGEMQAQDAMGYAAATAATATLPEADEMTSAGG 180	
Qy	121 LIATNLGONTPAIANNEAYGEMQAQDAMGYAAATAATATLPEADEMTSAGG 180	Db	121 LIATNLGONTPAIANNEAYGEMQAQDAMGYAAATAATATLPEADEMTSAGG 180	
Qy	181 LLEQQAEEBAASDTAAANQMLNNPQALQOQAQPTQGTPSSKGJLWKTSPHRSPLSN 240	Db	181 LLEQQAEEBAASDTAAANQMLNNPQALQOQAQPTQGTPSSKGJLWKTSPHRSPLSN 240	
Qy	241 MVSMANNNSMTNSCVSMNTLSSMLKGFPAAPAAAQVOTAAONGVRAMSSLGSSLGSSG 300	Db	241 MVSMANNNSMTNSCVSMNTLSSMLKGFPAAPAAAQVOTAAONGVRAMSSLGSSLGSSG 300	
Qy	241 MVSMANNNSMTNSCVSMNTLSSMLKGFPAAPAAAQVOTAAONGVRAMSSLGSSLGSSG 300	Db	241 MVSMANNNSMTNSCVSMNTLSSMLKGFPAAPAAAQVOTAAONGVRAMSSLGSSLGSSG 300	
Qy	301 LGGGYAANLGRAASVGSLSVPOAAWAANQAVTAAARALPLTSLSAERGPQMLGGLPV 360	Db	301 LGGGYAANLGRAASVGSLSVPOAAWAANQAVTAAARALPLTSLSAERGPQMLGGLPV 360	
Qy	361 GOMGARAGGGSGVLRPPRYPMPHSAAAG 391	Db	361 GOMGARAGGGSGVLRPPRYPMPHSAAAG 391	
Qy	361 GOMGARAGGGSGVLRPPRYPMPHSAAAG 391	Db	361 GOMGARAGGGSGVLRPPRYPMPHSAAAG 391	

RESULT 10
 AAE17571 ID AAE17571 standard; protein; 391 AA.
 XX AC AAE17571;
 XX DT 22-APR-2002 (first entry)
 DE Mycobacterium species MTB39 (TbH9) protein #2.
 XX KW Fusion protein; antigen; serological sensitivity; immune response;
 KW tuberculosis; infection; vaccine; MTB39; TbH9 protein.
 OS Mycobacterium sp.
 XX PN WO200198460-A2.
 XX PD 27-DEC-2001.
 XX DT 20-JUN-2001; 2001WO-US019359.
 XX DE Mycobacterium species MTB39 (TbH9) protein #2.
 XX KW Fusion protein; antigen; serological sensitivity; immune response;
 KW tuberculosis; infection; vaccine; MTB39; TbH9 protein.
 OS Mycobacterium sp.
 XX PN WO200198460-A2.
 XX PD 01-FEB-2001; 2000US-00597796.
 XX PA (CORI-) CORIXA CORP.
 XX PI Siekiy Y, Reed S, Alderson M;
 XX DR 2002-147798/19.

DR N-PSDB; AAD28341.
XX Composition comprising MTB39 antigen and MTB32A antigen from
XX Mycobacterium species, useful for eliciting immune response in a subject.
XX Claim 83; Page 102-103; 136pp; English.

XX The present invention relates to fusion proteins containing at least two
XX Mycobacterium species antigens, nucleotides encoding them and
XX compositions comprising such fusion proteins. The present invention
XX particularly relates to nucleic acids encoding fusion proteins that
XX include two or more individual M. tuberculosis antigens which increase
XX the serological sensitivity of sera from individuals infected with
XX tuberculosis and methods for their use in diagnosis, prevention and
XX treatment of tuberculosis infection. Sequences of the invention are
XX useful for eliciting an immune response in a mammal, e.g., human,
XX immunised with BCC. They are useful in the diagnosis, treatment and
XX prevention of Mycobacterium infection. The fusion proteins and the
XX polynucleotides are useful as diagnostic tools in patients infected with
XX Mycobacterium, in vitro and in vivo assays for detecting humoral
XX antibodies or cell-mediated immunity against M. tuberculosis, for the
XX diagnosis of infection or monitoring of disease progression, as
XX immunogens to generate or elicit a protective immune response in a
XX patient and for raising anti-M. tuberculosis antibodies in a non-human
XX animal. Sequences of the invention are also used as vaccines. MTB32A
XX fusion proteins of the invention are useful as in vivo diagnostic agents
XX for intradermal skin test. The present sequence is Mycobacterium species
XX MTB39 (TbH9) protein

Sequence 391 AA:

Query Match Best Local Similarity 100.0%; Score 1949; DB 5; Length 391;
 Pred. No. 1.2e-142; T=217

This sequence represents a recombinant *Mycobacterium tuberculosis* bi-carbonic anhydrase. It contains a 5' terminal sequence identical to the *M. tuberculosis* carboxylic anhydrase gene, followed by a 15 amino acid linker, and a C-terminal sequence identical to the *M. smegmatis* carboxylic anhydrase gene.

Y 1 MVDFGALPPEINSARMYAAQVRYAAAYETAGLTVPPPVIAENRAELMI 100
 Y 1 MVDFGALPPEINSARMYAAQVRYAAAYETAGLTVPPPVIAENRAELMI 100
 b 61 SSAGLMVAAASPYVAMSVTAGQABLETAQVRYAAAYETAGLTVPPPVIAENRAELMI 120
 Y 61 SSAGLMVAAASPYVAMSVTAGQABLETAQVRYAAAYETAGLTVPPPVIAENRAELMI 120
 b 61 SSAGLMVAAASPYVAMSVTAGQABLETAQVRYAAAYETAGLTVPPPVIAENRAELMI 120
 Y 121 LIATNLIGQNTPAIAVNEAEYGMWAAQDAAMFGYAAATAATLIPPEAEPMTSGG 180
 Y 121 LIATNLIGQNTPAIAVNEAEYGMWAAQDAAMFGYAAATAATLIPPEAEPMTSGG 180
 b 121 LIATNLIGQNTPAIAVNEAEYGMWAAQDAAMFGYAAATAATLIPPEAEPMTSGG 180

Sequence 596 AA;

		Query	Match	Score	DB 2;	Length
b	b	181 LLEQRAVEEASDTAAANQLMNVQALQIAOPTGGTIPSSKIGGLWKTVPSPRSPISN	240	100.0%	Score 1949; Pred. No. 2, 1e-142;	596
Y		241 MVSMAHHMSMTNSGYSMINTLSSMLKGFAAAQAVTAQNGVRAMSLGSSLGSG	300	Best Local Similarity	100.0%;保守性	
Y		241 MVSMAHHMSMTNSGYSMINTLSSMLKGFAAAQAVTAQNGVRAMSLGSSLGSG	300	Matches	391; Mismatches 0;	
b		301 LGGGVAAANLGRAASVCSLSVPOAWAANQAVTPAARALPLTSAAERGPGLMLGGIPV	360	1 MYDFGALPPEINSARMYAGPGSASLYAAAQMDSVSDLFSAASAFOSVYWGTLTYGSWIG	60	
Y		301 LGGGVAAANLGRAASVCSLSVPOAWAANQAVTPAARALPLTSAAERGPGLMLGGIPV	360	9 MYDFGALPPEINSARMYAGPGSASLYAAAQMDSVSDLFSAASAFOSVYWGTLTYGSWIG	68	
Db		361 GOMGARGGGLGSVLRVPPRIVMPHSIAAG	391	61 SSAGLMVAAASPVAAMSVTAQCAELTAQVRAAAAYETAYGLTTPPPVIAENRAELMI	120	
Y		361 GOMGARGGGLGSVLRVPPRIVMPHSIAAG	391	69 SSAGLMVAAASPVAAMSVTAQCAELTAQVRAAAAYETAYGLTTPPPVIAENRAELMI	128	
Db		121 LIATNLIGQNTPAIVNEAEYGMWAQDAAAAMFGYAAATAATATILLPFEEAPMTSAGG	180	121 LIATNLIGQNTPAIVNEAEYGMWAQDAAAAMFGYAAATAATATILLPFEEAPMTSAGG	180	
Y		129 LIATNLIGQNTPAIVNEAEYGMWAQDAAAAMFGYAAATAATATILLPFEEAPMTSAGG	188	129 LIATNLIGQNTPAIVNEAEYGMWAQDAAAAMFGYAAATAATATILLPFEEAPMTSAGG	188	
Db		181 LLEQAAAVEBEASTAAANQLMNVQALQIAOPTGGTIPSSKIGGLWKTVPSPRSPISN	240	181 LLEQAAAVEBEASTAAANQLMNVQALQIAOPTGGTIPSSKIGGLWKTVPSPRSPISN	240	
Y		189 LLEQAAAVEBEASTAAANQLMNVQALQIAOPTGGTIPSSKIGGLWKTVPSPRSPISN	248	189 LLEQAAAVEBEASTAAANQLMNVQALQIAOPTGGTIPSSKIGGLWKTVPSPRSPISN	248	
Db		241 MVSANNHMSMTNSGVSMNTLSSMLKGFAAAAQAVTAQNGVRAMSLGSSLGSG	300	241 MVSANNHMSMTNSGVSMNTLSSMLKGFAAAAQAVTAQNGVRAMSLGSSLGSG	300	
Y		249 MVSANNHMSMTNSGVSMNTLSSMLKGFAAAAQAVTAQNGVRAMSLGSSLGSG	308	249 MVSANNHMSMTNSGVSMNTLSSMLKGFAAAAQAVTAQNGVRAMSLGSSLGSG	308	
		RESULT 11				
		AY32070 standard; protein: 596 AA.				
	ID	AY32070				
	AC	AY32070;				
	DT	17-JAN-2000 (first entry)				
	XX	Mycobacterium tuberculosis antigen fusion protein MtbS9f.				

Qy	301	LGGSVAAANLGRAASVGSISLSPQAWAANQVTPARALPLTSLSAAERGPQMLGGIPV	360	Db	9	MVDGALPPEINSARNYAGPCSAASLVAAQNMDSYASD-LFSAASAFQSYVWGL-TVGSNIG	68
Db	309	LGGSVAAANLGRAASVGSISLSPQAWAANQVTPARALPLTSLSAAERGPQMLGGIPV	368	Qy	61	SSAGLMVAAASPYVAMSVTAGQELTAQVRAAVAAAYETAYGLTVPPVIAENRAELMTI	120
Qy	361	GOMGARAGGGLSGLSVLRLVPPRPPYVMPSPAAG	391	Db	69	SSAGLMVAAASPYVAMSVTAGQELTAQVRAAVAAAYETAYGLTVPPVIAENRAELMTI	128
Db	369	GOMGARAGGGLSGLSVLRLVPPRPPYVMPSPAAG	399	Qy	121	LJATNLIGQNTPAIAVNEGYGMWAQDAAMFGYAATAATATLPLFEAPEMTSAGG	180
RESULt 12				Db	129	LJATNLIGQNTPAIAVNEGYGMWAQDAAMFGYAATAATATLPLFEAPEMTSAGG	188
AAE29710	ID	AAE29710 standard; protein; 596 AA.		Qy	181	LLEQAAVEEASDTAAANOLMNVQPLQQLAQLOAOPTQTPSSKLGGKTKVSPHRSPSN	240
XX	AC	AAE29710;		Db	189	LLEQAAVEEASDTAAANQLMNVQPLQQLAQLOAQPQGTTPSSKLGGKTKVSPHRSPSN	248
XX	XX	29-AUG-2003 (revised)		Qy	241	MVSMAHHMSMTNSGVSMNTNLSSMLKGFPAPAAAQVYOTAQNGVRAMSISLSSLGSSG	300
DT	DT	27-JAN-2003 (first entry)		Db	249	MVSMAHHMSMTNSGVSMNTNLSSMLKGFPAPAAAQVYOTAQNGVRAMSISLSSLGSSG	308
XX	DE	Mycobacterium sp. MTB9F fusion protein.		Qy	301	LGGGVAAANLGRAASVGSISLSPQAMAAANQVTPARALPLTSLSAAERGPQMLGGIPV	360
XX	KW	Vaccine; immunity; diagnostic agent; gene therapy; TbH9; antigen; Ra35;		Db	309	LGGGVAAANLGRAASVGSISLSPQAMAAANQVTPARALPLTSLSAAERGPQMLGGIPV	368
XX	KW	MTB9F; fusion protein.		Qy	361	QMGARGAGGLSGLSVLRLVPPRPPYVMPSPAAG	391
OS	OS	Mycobacterium sp.		Db	369	QMGARGAGGLSGLSVLRLVPPRPPYVMPSPAAG	399
OS	OS	Mycobacterium tuberculosis.					
XX	XX	Chimeric.					
PN	PN	WO20027792-A2.					
XX	PD	19-SEP-2002.					
XX	XX	13-MAR-2002; 2000WO-US008223.					
PF	PF	13-MAR-2001; 2001US-0275837P.					
XX	PR	13-MAR-2001; 2001US-0275837P.					
XX	XX	(CORI-) CORIXA CORP.					
PA	PA	(CORI-) CORIXA CORP.					
XX	PI	Skeiky Y., Brannon M., Guderian J.					
XX	XX	WPI: 2002-759844/82.					
DR	DR	N-PSDB; AAD47086.					
XX	XX	PT M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.					
XX	XX	PT New recombinant nucleic acid molecule comprising a Leishmania tsa, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.					
XX	XX	PT Disclosure; Page 98-99; 155pp; English.					
PS	PS	PT The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigenic or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from tSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium tuberculosis. This fusion protein comprises Ra35 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)					
XX	XX	CC The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigenic or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from tSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium tuberculosis. This fusion protein comprises Ra35 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)					
XX	XX	CC Sequence 596 AA;					
CC	CC	CC Query Match 100.0%; Score 1919; DB 5; Length 596;					
CC	CC	CC Best Local Similarity 100.0%; Pred. No. 2.1e-142; Mismatches 0; Indels 0; Gaps 0;					
CC	CC	CC 1 MVDGALPPEINSARNYAGPPGSASLVAAQNWDSVASDLFSAASFQSYVWGL-TVGSNIG	60	Qy			

immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines, MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB59F (Tbh9-Ra35) fusion protein.

Sequence 596 AA:

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Query Match          100.0%; Score 1949; DB 5; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.1e-142; Indels 0; Gaps 0;
Matches 391; Conservative 0; Mismatches 0; Gaps 0;
PPI: 2002.17134/22.
WPI: ABK143.9.

Qy   1  MVDGFALPPEINSARMYAGPGSASIVAAQMDSVASLFSASAPOSVWGLTVGSWIG 60
Db    9  MVDGFALPPEINSARMYAGPGSASIVAAQMDSVASLFSASAPOSVWGLTVGSWIG 68
Qy   61  SSACGLMVAANASPYTAMSVTAGELTAQVRLVAAATNTAGLTTPPVIAENRAELMI 120
Db   69  SSACGLMVAANASPYTAMSVTAGELTAQVRLVAAATNTAGLTTPPVIAENRAELMI 128
Qy   121 LIATNLIGGNTPATAVNEAEYGNWQAQDAAMMEGAATAATATLIPFEAPMTSAGG 180
Db   129 LIATNLIGGNTPATAVNEAEYGNWQAQDAAMMEGAATAATATLIPFEAPMTSAGG 188
Qy   181 LLEQAAAYEASDITAANCLMNVPQQLAQOPTGTTPSXLGIWKTSPHRSPISN 240
Db   189 LLEQAAAYEASDITAANCLMNVPQQLAQOPTGTTPSXLGIWKTSPHRSPISN 248
Qy   241 MVSQANHNSIMTSVGSMNTLSSMLKGSSGTTAONGYRAMSSLGSSGSSG 300
Db   249 MVSQANHNSIMTSVGSMNTLSSMLKGSSGTTAONGYRAMSSLGSSGSSG 308
Qy   301 LGGGYAANILGRAASVGSLSVPOWAANQAVTAAPARALPLTSLSAABRGQQLGSLPV 360
Db   309 LGGGYAANILGRAASVGSLSVPOWAANQAVTAAPARALPLTSLSAABRGQQLGSLPV 368
Qy   361 GQMGRAGGGSLGVLRVPRPYMPHSPAAAG 391
Db   369 GQMGRAGGGSLGVLRVPRPYMPHSPAAAG 399

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RESULT 14
AAU74599 standard: protein; 599 AA.

XX

AAU74599;

DT 29-AUG-2003 (revised)

DT 08-MAY-2002 (first entry)

XX Antigenic fusion protein Tb59-Ra35 (Mt59E).

XX Fusion protein; tuberculosis; immunogen; vaccine; Tb59-Ra35; Mt59E.

XX Mycobacterium tuberculosis.

XX Chimeric.

FH Key Location/Qualifiers

FT Misc-difference 597

FT /label= OTHER

FT /note= "OTHER= Xaa. Xaa= In frame stop codon"

XX US2002009459-A1.

XX 24-JAN-2002.

PJ

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XX 07-APR-1999; 99US-00287849.
XX PR 13-MAR-1997; 97US-00818112.
XX PR 01-OCT-1997; 97US-00142578.
XX PR 18-FEB-1998; 98US-00025197.
XX PR 07-APR-1998; 98US-00056556.
XX PR 30-DEC-1998; 98US-00223040.
XX PA (REED/) REED S G.
PA (SKEIKY/) SKEIKY Y A.
PA (DILL/) DILLON D C.
PA (ALDERON/) ALDERON M.
PA (CAMPO/) CAMPOS-NETO A.
XX Reed SG, Skeiky YA, Dillon DC, Alderson M, Campos-Neto A;
PI XX Campos-Neto A;
DR XX DR N-FSBB; ABK143.9.

Claim 1: Fig 12; 62pp; English.

The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX PS Claim 1; Fig 12; 62pp; English.
XX Sequence 599 AA;

Query Match          100.0%; Score 1949; DB 5; Length 599;
Best Local Similarity 100.0%; Pred. No. 2.1e-142;
Matches 391; Conservative 0; Mismatches 0; Gaps 0;
PPI: 2002.17134/22.
WPI: ABK143.9.

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Db    9  MVDGFALPPEINSARMYAGPGSASIVAAQMDSVASLFSASAPOSVWGLTVGSWIG 68
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Db   69  SSACGLMVAANASPYTAMSVTAGELTAQVRLVAAATNTAGLTTPPVIAENRAELMI 128
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Db   129 LIATNLIGGNTPATAVNEAEYGNWQAQDAAMMEGAATAATATLIPFEAPMTSAGG 188
Qy   181 LLEQAAAYEASDITAANCLMNVPQQLAQOPTGTTPSXLGIWKTSPHRSPISN 240
Db   189 LLEQAAAYEASDITAANCLMNVPQQLAQOPTGTTPSXLGIWKTSPHRSPISN 248
Qy   241 MVSQANHNSIMTSVGSMNTLSSMLKGSSGTTAONGYRAMSSLGSSGSSG 300
Db   249 MVSQANHNSIMTSVGSMNTLSSMLKGSSGTTAONGYRAMSSLGSSGSSG 308
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Db   309 LGGGYAANILGRAASVGSLSVPOWAANQAVTAAPARALPLTSLSAABRGQQLGSLPV 368
Qy   361 GQMGRAGGGSLGVLRVPRPYMPHSPAAAG 391
Db   369 GQMGRAGGGSLGVLRVPRPYMPHSPAAAG 399

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RESULT 15

AYY32068 standard; protein; 600 AA.
 ID AYY32068:
 XX
 AC AYY32068:
 XX DT 17-JAN-2000 (first entry)
 XX Mycobacterium tuberculosis antigen protein Mtb61f.
 DEB
 XX Tuberculosis; antigen; fusion protein; Mtb61f; TbH9; DPV; MTI; diagnosis;
 KW therapy; vaccine; immunogen.
 XX OS Mycobacterium tuberculosis.
 XX WC9951748-A2.
 PN XX PD 14-OCT-1999.
 XX PP 07-APR-1999; 99RC-US007717.
 XX PR 07-APR-1998; 98US-00056556.
 PR 30-DEC-1998; 98US-00223040.
 XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Alderson M, Campos-Neto A;
 XX DR WPI: 1999-601610/51.
 DR N-PsDB; AAZ20203.
 XX PT New fusion proteins useful for diagnosis, prevention and treatment of
 PT tuberculosis.
 XX PT
 PS Claim 1; Fig 10A-B; 83pp; English.
 XX CC This sequence represents a recombinant Mycobacterium tuberculosis tri-
 CC antigen fusion protein, termed Mt61f, composed of the antigens TbH9, DPV
 CC and MTI. The fusion protein is expressed in host cells using a vector
 CC carrying a polynucleotide (see AAZ20203) comprising the coding sequences
 CC for the 3 antigens. The inventors provide the coding sequences for
 CC 71 containing at least 2 M. tuberculosis antigens. The new fusion
 CC proteins and polynucleotides encoding them are useful as vaccines for
 CC preventing tuberculosis (claimed), for diagnosis (via in vitro assays or
 CC intradermal skin tests for detection of anti-M. tuberculosis antibodies),
 CC monitoring of disease progression, and treatment of tuberculosis. They
 CC are more effective immunogens than mixtures of the individual protein
 XX SQ Sequence 600 AA;

Qy	Db								
Oy	301	Oy	360	Oy	361	Oy	369	Oy	391
Db	309	Db	369	Db	369	Db	369	Db	399

Search completed: August 25, 2004, 03:10:27
 Job time : 131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2004, 03:08:19 ; Search time 34 Seconds
(without alignments)

593,699 Million cell updates/sec

Title: US-09-724-685-107

Perfect score: 1949

Sequence: 1 MVDEGALPPEINSARMYACP.....SGVILRVPBRPYVMPHSPAAAG 391

Scoring table: BL03UN62

Gapext 10.0 , Gapext 0.5

Searched: 389414 seqs., 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cn2_6_ptodata/2/iaa/5B_COMB.pep:/*
3: /cn2_6_ptodata/2/iaa/6A_COMB.pep:/*
4: /cn2_6_ptodata/2/iaa/6B_COMB.pep:/*
5: /cn2_6_ptodata/2/iaa/FACTUS_COMB.pep:/*
6: /cn2_6_ptodata/2/iaa/backfile.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1949	100.0	391	3	US-09-818-112-107- 20	Sequence 107, APP
2	1949	100.0	391	4	US-09-818-111-102- 20	Sequence 102, APP
3	1949	100.0	391	4	US-09-072-596-102- 20	Sequence 102, APP
4	1949	100.0	391	4	US-09-072-967-107- 20	Sequence 107, APP
5	1949	100.0	391	4	US-09-287-849-26- 20	Sequence 26, APP
6	1949	100.0	596	4	US-09-287-849-22- 20	Sequence 22, APP
7	1949	100.0	600	4	US-09-223-040-2	Sequence 2, APP
8	1944	99.7	729	4	US-09-287-849-2	Sequence 2, APP
9	1944	99.7	729	4	US-09-287-849-2	Sequence 2, APP
10	1652.5	84.8	396	3	US-09-818-112-111	Sequence 111, APP
11	1652.5	84.8	396	4	US-09-818-111-106	Sequence 106, APP
12	1652.5	84.8	396	4	US-09-056-556-111	Sequence 111, APP
13	1652.5	84.8	396	4	US-09-072-596-106	Sequence 106, APP
14	1652.5	84.8	396	4	US-09-072-967-111	Sequence 111, APP
15	1486.5	76.3	359	3	US-09-818-112-109	Sequence 109, APP
16	1486.5	76.3	359	4	US-09-818-111-104	Sequence 104, APP
17	1486.5	76.3	359	4	US-09-056-556-109	Sequence 109, APP
18	1486.5	76.3	359	4	US-09-072-596-104	Sequence 104, APP
19	1486.5	76.3	359	4	US-09-072-967-109	Sequence 109, APP
20	1187.5	60.9	358	4	US-09-287-849-8	Sequence 8, APP
21	1187.5	60.9	263	3	US-09-818-112-91	Sequence 91, APP
22	1187	60.9	263	4	US-09-818-111-92	Sequence 92, APP
23	1187	60.9	263	4	US-09-056-556-91	Sequence 91, APP
24	1187	60.9	263	4	US-09-072-596-92	Sequence 92, APP
25	1187	60.9	263	4	US-09-072-967-91	Sequence 91, APP
26	766.5	39.3	400	4	US-09-073-009-126	Sequence 126, APP
27	766.5	39.3	400	4	US-09-073-010-126	Sequence 126, APP

ALIGNMENTS

RESULT 1
US-09-818-112-107
; Sequence 107 Application US/08918112
; Patent No. 6220969
; GENERAL INFORMATION:
; / APPLICANT: Reed, Steven G.
; / APPLICANT: Skalky, Yasir A.W.
; / APPLICANT: Campos-Neto, Antonio
; / APPLICANT: Dillon, Davin C.
; / APPLICANT: Houghton, Raymond
; / APPLICANT: Vecwick, Thomas S.
; / APPLICANT: Twardzik, Daniel R.
; / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; / NUMBER OF SEQUENCES: 153
; / CORRESPONDENCE ADDRESS:
; / ADDRESSEE: SEED and BERRY LLP
; / STREET: 6300 Columbia Center, 701 Fifth Avenue
; / CITY: Seattle
; / STATE: Washington
; / COUNTRY: USA
; / ZIP: 98104-7092
; / COMPUTER READABLE FORM:
; / MEDIUM TYPE: Floppy disk
; / COMPUTER: IBM PC compatible
; / OPERATING SYSTEM: PC-POS/MS-DOS
; / SOFTWARE: Patent In Release #1.0, Version #1.30
; / CURRENT APPLICATION DATA:
; / APPLICATION NUMBER: US/08/818,112
; / FILING DATE: 13-MAR-1997
; / CLASSIFICATION: 424
; / ATTORNEY/AGENT INFORMATION:
; / NAME: Makki, David J.
; / REGISTRATION NUMBER: 31,392
; / REFERENCE DOCKET NUMBER: 210121:411C6
; / TELECOMMUNICATION INFORMATION:
; / TELEPHONE: (206) 622-4300
; / TELEFAX: (206) 682-6031
; / INFORMATION FOR SEQ ID NO: 107:
; / SEQUENCE CHARACTERISTICS:
; / LENGTH: 391 amino acids
; / TYPE: amino acid
; / STRANDEDNESS: single
; / TOPOLOGY: linear
; / US-09-818-112-107
; / Query Match Score 1949; DB 3;
; / Best Local Similarity 100%; Pred. No. 2.9e-154;
; / Matches 391; Conservative 0; Mismatches 0;
; / Indels 0; Gaps 0;

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 Database 1 MVDFGALPBEINSARMYAGPGSASLVAQAMQDSVASDLSASAFAQSVMGLTVGSWIG 60
 US-09-072-596-102

RESULT 4
 US-09-072-596-102
 Sequence 10/10, Application US/09072596
 Patent No. 6458336
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.R.
 APPLICANT: Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072.596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
 INFORMATION FOR SEO ID NO: 102:
 LENGTH: 391 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPology: linear
 US-09-072-596-102

Query Match 100.0% Score 1949; DB 4; Length 391;
 Best Local Similarity 100.0% Pred. No. 2.9e-154;
 Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Database 1 MVDFGALPBEINSARMYAGPGSASLVAQAMQDSVASDLSASAFAQSVMGLTVGSWIG 60
 US-09-072-596-102

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 Database 121 LIATNLGGNTPAIAVNELEYGENWAQDAAMGYAAATAATATLIPPEAPEMTSAG 180
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 Database 181 LLQQAAAVEEAEASDAAQOLMNNPQALQOLAOPTGTTSSKLGWIKTVSPHRSPISN 240
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 Database 241 MVSMANNHSMTNMGVSMTNTLSMLKGKAPAAAQAQVTAQNGVAMSSLGSSG 300
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 Database 301 LGGGYAANIGRAASYGSLSYPOQWAANQAVTPAARALPITSUTSAERGPQMLGGLPV 360
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RESULT 5
 US-09-072-967-107
 Sequence 10/10, Application US/09072967
 Patent No. 6552877
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.R.
 APPLICANT: Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072.596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900

FILING DATE: 05-MAY-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEX/FAX: (206) 682-6331
 INFORMATION FOR SEQ ID NO: 107:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 US-09-27-967-107

Query Match 100.0%; Score 1949; DB 4; Length 391;
 Best Local Similarity 100.0%; Prod. No. 2.9e-154; Mismatches 0; Indels 0; Gaps 0;
 Matches 391; Conservative 0; Features 0;

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 Db 1 MVDFGALPPINSARMYAGGSASLVAQVRAAATAGVLTAGVLTGSGWIG 68

Qy 1 MVDFGALPPINSARMYAGGSASLVAQVRAAATAGVLTAGVLTGSGWIG 60
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Qy 61 SSAGIMVAAASPYYAMSVTAQGELTAQVRAAATAGVLTAGVLTGSGWIG 120
 Db 61 SSAGIMVAAASPYYAMSVTAQGELTAQVRAAATAGVLTAGVLTGSGWIG 120

Qy 121 LIATNLGQNTPAIVNEAEGYGEWAQDAAMFGSYAAATAATATLIPPEAPEMTSAGG 180
 Db 121 LIATNLGQNTPAIVNEAEGYGEWAQDAAMFGSYAAATAATLIPPEAPEMTSAGG 180

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Qy 361 QGMGARGGGSLGVLPVPRPYMPHSPIAG 391
 Db 369 QGMGARGGGSLGVLPVPRPYMPHSPIAG 399

RESULT 6
 US-09-287-849-26
 Sequence 26, Application US/09287849
 Patent No. 6627198

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skelky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Alderson, Mark
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Corixa Corporation
 TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 FILE REFERENCE: 014058-0090201US
 CURRENT FILING DATE: 1999-04-07
 PRIOR APPLICATION NUMBER: US/09/287,849
 CURRENT FILING DATE: 1997-03-13
 PRIOR APPLICATION NUMBER: US/09/2,578
 CURRENT FILING DATE: 1997-10-01
 PRIOR APPLICATION NUMBER: US/09/025,197
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US/09/056,556
 PRIOR FILING DATE: 1998-04-07
 PRIOR APPLICATION NUMBER: US/09/223,040
 PRIOR FILING DATE: 1998-12-30
 NUMBER OF SEQ ID NOS: 46

RESULT 7
 US-09-287-849-22
 Sequence 22, Application US/09287849
 Patent No. 6627198

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skelky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Alderson, Mark
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Corixa Corporation
 TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 FILE REFERENCE: 014058-0090201US
 CURRENT FILING DATE: 1999-04-07
 PRIOR APPLICATION NUMBER: US/08/818,112
 CURRENT FILING DATE: 1997-03-13
 PRIOR APPLICATION NUMBER: US/08/942,578
 CURRENT FILING DATE: 1997-10-01
 PRIOR APPLICATION NUMBER: US/09/025,197
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US/09/056,556
 PRIOR FILING DATE: 1998-04-07
 PRIOR APPLICATION NUMBER: US/09/223,040
 PRIOR FILING DATE: 1998-12-30
 NUMBER OF SEQ ID NOS: 46

SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: PRT;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
; US-09-287-840-22

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Best Local Similarity 100.0% Pred. No. 5 2e-154; Indels 0; Gaps 0;
Matches 391; Conservative 0; Mismatches 0;

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Db 9 MVDFGALPBEINSARMYAGPGSASLVAQQMWDVSASDLSAASAFAQSVWGLTVGSWIG 68

Qy 121 LIATNLGGONTPAVNEAYGENWAQDAAMGYAALTATAATLPEEPEAPMTSAGG 180
Db 129 LIATNLGGONTPAVNEAYGENWAQDAAMGYAALTATAATLPEEPEAPMTSAGG 188

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Db 189 LLEQAAYEEASDTAAANQMLNNYQALQOLAOPTOGTTPSSKGIGLWKTVPSPRSPI SN 248

RESULT 9
US-09-287-849-2
; Sequence 2, Application US/09287849
; Patent No. 662198

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Db 249 MVSVANNHSMTNSGYSMTNTLSSMLKGAPAQAQAVTAQNGVRAMSSLGSSG 308

Qy 301 LGGGYAANLGRAASYGSLSVPOQAAAANGDAVTPAARALPLTSLTSAAERGPQMLGSLPV 360
Db 309 LGGGYAANLGRAASYGSLSVPOQAAAANGDAVTPAARALPLTSLTSAAERGPQMLGSLPV 368

Qy 361 GOMGARAGGGLSGVLRVPPRPPYMPHSPIAG 391
Db 369 GOMGARAGGGLSGVLRVPPRPPYMPHSPIAG 399

RESULT 8
US-09-223-040-2
; Sequence 2, Application US/09223040
; Patent No. 6544522
; GENERAL INFORMATION:
; APPLICANT: Skelley, Yasir
; PRIOR ART: Alderson, Mark
; APPLICANT: Campos-Nero, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE REFERENCE: 014058-009010JS
; CURRENT APPLICATION NUMBER: US/09/223,040
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 729
; TYPE: PRT;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
; US-09-223-040-2

Query Match 99.7% Score 1944; DB 4; Length 729;
Best Local Similarity 99.7% Pred. No. 1.8e-153; Indels 0; Gaps 0;
Matches 390; Conservative 0; Mismatches 1;

Qy 1 MVDFGALPBEINSARMYAGPGSASLVAQQMWDVSASDLSAASAFAQSVWGLTVGSWIG 60
Db 142 MVDFGALPBEINSARMYAGPGSASLVAQQMWDVSASDLSAASAFAQSVWGLTVGSWIG 201

Qy 61 SSAGLMVAAASPYVAMSVTAGQELTAQVRAAAAYETAYGLTVPPVIAENRAELMI 120
Db 202 SSAGLMVAAASPYVAMSVTAGQELTAQVRAAAAYETAYGLTVPPVIAENRAELMI 261

Query Match Score 1652.5; DB 4; Length 396;
 Best Local Similarity 84.9%; Pred. No. 1.4e-129;
 Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;
 Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;

Qy 1 MYDFGALPPEINSARMYAGPGSASLVAQAAKMDVSASDLFSAASAQSVMGLTVGSWIG 60
 Db 1 VVDGALPPEINSARMYAGPGSASLVAQAAKMDVSASDLFSAASAQSVMGLTVGSWIG 60
 Qy 61 SSAGLMVAAASPYAMSVTAQGAELTAAQVRVAAAAYETAYGLTPPPVIAENRAELMI 120
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 Db 121 LIATNLGGCTPAIAVNAAEYGENWQAQAAVATAATATLPPPEAPEMTSAGG 180
 Qy 121 LIATNLGGCTPAIAVNAAEYGENWQAQAAVATAATATLPPPEAPEMTSAGG 180
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 Qy 181 LLEAAAVEEAASDTAAANQLMNVPOALQOALOPTGTTSSKLGWKTVPHRSPISN 240
 Db 181 LLEQAVAAVEEEAIDTAANQLMNVPOALQOALOPTGTTSSKLGWKTVPHRSPISN 240
 Qy 241 MVSZANNHNSMTNSGVSMINTLSSMLKGFAAAAAAQVTAQNGVRAMSS ---LGSSL 296
 Db 241 IVSMANNHNSMTNSGVSMINTLSSMLKGFAAAAAAQVTAQNGVRAMSS ---LGSSL 296
 Qy 297 GSSGLGGVAAANLGRASVGSLSYPOAWAANAOAVTPARALPLTSLSAARGPGOMLG 356
 Db 300 GSSGLGAGTAANLGRASVGSLSYPOAWAANAOAVTPARALPLTSLSAQTAPGHMLG 359
 Qy 357 GLPVQMGARAG - GGLSGVLRVPPRPMPHSPAAG 391
 Db 360 GLPLQQLTNSGGGFGGSNALRMPFRAYMFRVPAAG 396

RESULT 12
 US-09-056-556-111
 Sequence 111; Application US/09056556

Patent No. 635056
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND TREATMENT OF SEQUENCES: 241
 NUMBER OF SEQUENCES: 241
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-1092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/056,556
 FILING DATE: 07-APR-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 111:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

Query Match Score 1652.5; DB 4; Length 396;
 Best Local Similarity 84.8%; Pred. No. 1.4e-129;
 Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;
 Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;

Qy 1 MYDFALPPEINSARMYAGPGSASLVAQAAKMDVSASDLFSAASAQSVMGLTVGSWIG 60
 Db 1 VVDGALPPEINSARMYAGPGSASLVAQAAKMDVSASDLFSAASAQSVMGLTVGSWIG 60
 Qy 61 SSAGLMVAAASPYAMSVTAQGAELTAAQVRVAAAAYETAYGLTPPPVIAENRAELMI 120
 Db 61 SSAGLMVAAASPYAMSVTAQGAELTAAQVRVAAAAYETAYGLTPPPVIAENRAELMI 120
 Db 121 LIATNLGGCTPAIAVNAAEYGENWQAQAAVATAATATLPPPEAPEMTSAGG 180
 Qy 121 LIATNLGGCTPAIAVNAAEYGENWQAQAAVATAATATLPPPEAPEMTSAGG 180
 Db 181 LLEQAVAAVEEEAIDTAANQLMNVPOALQOALOPTGTTSSKLGWKTVPHRSPISN 240
 Qy 181 LLEQAVAAVEEEAIDTAANQLMNVPOALQOALOPTGTTSSKLGWKTVPHRSPISN 240
 Db 241 IVSMANNHNSMTNSGVSMINTLSSMLKGFAAAAAAQVTAQNGVRAMSS ---LGSSL 296
 Qy 241 IVSMANNHNSMTNSGVSMINTLSSMLKGFAAAAAAQVTAQNGVRAMSS ---LGSSL 296
 Db 297 GSSGLGGVAAANLGRASVGSLSYPOAWAANAOAVTPARALPLTSLSAARGPGOMLG 356
 Qy 297 GSSGLGGVAAANLGRASVGSLSYPOAWAANAOAVTPARALPLTSLSAARGPGOMLG 356
 Db 300 GSSGLGAGTAANLGRASVGSLSYPOAWAANAOAVTPARALPLTSLSAQTAPGHMLG 359
 Qy 357 GLPVQMGARAG - GGLSGVLRVPPRPMPHSPAAG 391
 Db 360 GLPLQQLTNSGGGFGGSNALRMPFRAYMFRVPAAG 396

RESULT 13
 US-09-072-596-106
 Sequence 13; Application US/09072596
 Paten No. 6458365
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Nato, Antonia
 APPLICANT: Houghton, Raymond
 APPLICANT: Verdiuk, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 3500
 CORRESPONDENCE ADDRESS:
 ADDRESS: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-1092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 111:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

INFORMATION FOR SEQ ID NO: 106:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLGY: linear
 09-072-598-106

Inquiry Match Score 1652.5; DB 4; Length 396;
 Best Local Similarity 84.8%; Pred. No. 1.4e-129; Indels 7; Gaps 3;
 Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;

1 MVDFGALPPEINSARMVAGPGSASLVAQAMWDSVASDLFSSASAFAOSVWGLTGSWIG 60
 1 VVDFGALPPEINSARMVAGPGSASLVAQAMWDSVASDLFSSASAFAOSVWGLTGSWIG 60

61 SSAGLMYAAASPPTAMSVTAGOELPAQTVRAAAYETAYGLTPPPVIAENRAELMI 120
 61 SSAGLMYAAASPPTAMSVTAGOELPAQTVRAAAYETAYGLTPPPVIAENRAELMI 120

121 LIATNLGQNTPIAVNEAEYGMWAAQDAAMFGYAATAATATLPLPEAPEMTSAGG 180
 121 LIATNLGQNTPIAVNEAEYGMWAAQDAAMFGYAATAATEALLPEDAPLTNPCC 180

181 LIEQAAAVEREASTTAANQLQNNVPQLQLAQOPTCTTSSKLGEGWKTVSPHRSPIIN 240
 181 LIEQAAAVEREALDTAAANQLQNNVPQLQLAQOPTSIWPFDQSELWKAQPHSPLSN 240

241 MVSMMANNHSMTNGSVMSMTLSSMLKGFPAPAAAQAVQTAQONGYRAMSS---LGSSU 296
 241 IVSMLNHHSMTNGSVMSMTLSSMLKGFP-AAAQAVETQAQNGYQAMSSLGQSSL 299

297 GSSGLGGVAAANLGRASVGSLSVQAWAAANQAVTPAARALPLTSITSAERGQMLG 356
 300 GSSGLGGVAAANLGRASVGSLSVQAWAAANQAVTPAARALPLTSITSAQTAQHMLG 359

357 GLPVQMGARAG-GGLSGURVPPRPPVMPHSPIAG 391
 360 GLPLGQLTNSGGGFGCGYSNALRMPHPRAYVMBRVPAAG 396

RESULT 14
 Sequence 111, Application US/09072-967-111
 Patent No. 652877
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skerly, Yasir A.W.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,967
 FILING DATE: 05-MAY-1998

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121-411C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-6900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 111:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLGY: linear
 US-09-072-967-111

Query Match Score 1652.5; DB 4; Length 396;
 Best Local Similarity 84.9%; Pred. No. 1.4e-129; Mismatches 34; Indels 7; Gaps 3;

Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;

1 MVDFGALPPEINSARMVAGPGSASLVAQAMWDSVASDLFSSASAFAOSVWGLTGSWIG 60
 1 VVDFGALPPEINSARMVAGPGSASLVAQAMWDSVASDLFSSASAFAOSVWGLTGSWIG 60

61 SSAGLMYAAASPPTAMSVTAGOELPAQTVRAAAYETAYGLTPPPVIAENRAELMI 120
 61 SSAGLMYAAASPPTAMSVTAGOELPAQTVRAAAYETAYGLTPPPVIAENRAELMI 120

121 LIATNLGQNTPIAVNEAEYGMWAAQDAAMFGYAATAATATLPLPEAPEMTSAGG 180
 121 LIATNLGQNTPIAVNEAEYGMWAAQDAAMFGYAATAATEALLPEDAPLTNPCC 180

181 LIEQAAAVEREASTTAANQLQNNVPQLQLAQOPTCTTSSKLGEGWKTVSPHRSPIIN 240
 181 LIEQAAAVEREALDTAAANQLQNNVPQLQLAQOPTSIWPFDQSELWKAQPHSPLSN 240

241 MVSMMANNHSMTNGSVMSMTLSSMLKGFPAPAAAQAVQTAQONGYRAMSS---LGSSU 296
 241 IVSMLNHHSMTNGSVMSMTLSSMLKGFP-AAAQAVETQAQNGYQAMSSLGQSSL 299

297 GSSGLGGVAAANLGRASVGSLSVQAWAAANQAVTPAARALPLTSITSAERGQMLG 356
 300 GSSGLGGVAAANLGRASVGSLSVQAWAAANQAVTPAARALPLTSITSAQTAQHMLG 359

357 GLPVQMGARAG-GGLSGURVPPRPPVMPHSPIAG 391
 360 GLPLGQLTNSGGGFGCGYSNALRMPHPRAYVMBRVPAAG 396

RESULT 15
 US-09-072-967-111
 Sequence 111, Application US/09072-967-111
 Patent No. 652877
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skerly, Yasir A.W.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,967
 FILING DATE: 05-MAY-1998

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121-411C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-6900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 111:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLGY: linear
 US-09-072-967-111

Query Match Score 1652.5; DB 4; Length 396;
 Best Local Similarity 84.9%; Pred. No. 1.4e-129; Mismatches 34; Indels 7; Gaps 3;

Matches 337; Conservative 19; Mismatches 34; Indels 7; Gaps 3;

1 MVDFGALPPEINSARMVAGPGSASLVAQAMWDSVASDLFSSASAFAOSVWGLTGSWIG 60
 1 VVDFGALPPEINSARMVAGPGSASLVAQAMWDSVASDLFSSASAFAOSVWGLTGSWIG 60

61 SSAGLMYAAASPPTAMSVTAGOELPAQTVRAAAYETAYGLTPPPVIAENRAELMI 120
 61 SSAGLMYAAASPPTAMSVTAGOELPAQTVRAAAYETAYGLTPPPVIAENRAELMI 120

121 LIATNLGQNTPIAVNEAEYGMWAAQDAAMFGYAATAATATLPLPEAPEMTSAGG 180
 121 LIATNLGQNTPIAVNEAEYGMWAAQDAAMFGYAATAATEALLPEDAPLTNPCC 180

181 LIEQAAAVEREASTTAANQLQNNVPQLQLAQOPTCTTSSKLGEGWKTVSPHRSPIIN 240
 181 LIEQAAAVEREALDTAAANQLQNNVPQLQLAQOPTSIWPFDQSELWKAQPHSPLSN 240

241 MVSMMANNHSMTNGSVMSMTLSSMLKGFPAPAAAQAVQTAQONGYRAMSS---LGSSU 296
 241 IVSMLNHHSMTNGSVMSMTLSSMLKGFP-AAAQAVETQAQNGYQAMSSLGQSSL 299

297 GSSGLGGVAAANLGRASVGSLSVQAWAAANQAVTPAARALPLTSITSAERGQMLG 356
 300 GSSGLGGVAAANLGRASVGSLSVQAWAAANQAVTPAARALPLTSITSAQTAQHMLG 359

357 GLPVQMGARAG-GGLSGURVPPRPPVMPHSPIAG 391
 360 GLPLGQLTNSGGGFGCGYSNALRMPHPRAYVMBRVPAAG 396

RESULT 15
 US-09-072-967-111
 Sequence 111, Application US/09072-967-111
 Patent No. 652877
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Skerly, Yasir A.W.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Hendrickson, Ronald C.
 APPLICANT: Campos-Neto, Antonio
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
 NUMBER OF SEQUENCES: 355
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,967
 FILING DATE: 05-MAY-1998

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/818,112
 FILING DATE: 13-MAR-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.411C6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 109:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-818-112-109

Query Match 76.3% Score 1486.5; DB 3; Length 359;
 Best Local Similarity 84.2%; Pred. No. 7.9e-116; Gaps 2;
 Matches 303; Conservative 16; Mismatches 36; Indels 5;

Qy	1 MVDFGALPBEINSARMYAGPGSASLVAQQMWDVASDLSASAFSVVWGLTVWSWIG 60
Db	1 VVDGALPFEINSARMYAGPGSASLVAQKMDSVASDLSASAFSVVWGLTVWSWIG 60
Qy	61 SSAGLIMVAASPYAAMSVTAGQELTAAQVRAAAAYETAYGLTVBPPVIAENRAELMI 120
Db	61 SSAGLIMAAASPYAAMSVTAGQQLTAQVRAAAAYETAYRLTVBPPVIAENRFLMT 120
Qy	121 LIATNLIGGNTPAFVNPEYGMWQDAAMIGYAATAATATATATLIPFEAPEMTSAGG 180
Db	121 LTATNLGGNTPAFQNQAYSQNWQDQEAMGYAATAATEALIPFEDPLTPGG 180
Qy	181 LLEQAAAVEASDTAAANOLMNNVPQALQLAQPTGTTPSKLGGLWKTVSPHRSPISN 240
Db	181 LLEQAVAVPEAIDPAANQLMNNVPQALQLAQPAQGTPSSKLGGIWTAVSPHLSPLSN 240
Qy	241 MVSIMANNHNSMTNSGVSMNTLSSMLKGDPAAAQAVOTRAONGDAMSS---LGSSL 296
Db	241 VSSTANNHNSMMGTGVSMNTLHSMLKGIAAP-AAAQAVETAENGWAMSSLGSQGSSL 299
Qy	297 GSSGIGGGTAAANLGRAASTGSLSYPOANVAAQVTPARALPLTSITSAERGPGOMLG 356
Db	300 GSSGLGAGVAAANLGRAASTGSLSYPOANVAAQVTPARALPLTSITSAQTAPGHMLG 359

Search completed: August 25, 2004, 03:14:26

Job time : 36 secs

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